

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2005, 08:45:51 ; Search time 40 Seconds
(without alignments)
610.976 Million cell updates/sec

Title: US-09-895-814-525
Perfect score: 1369
Sequence: 1 MATAGNPGWFLGYLILGVA.....GVYTNLCRFTWEIKTVQAS 254

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	567.5	41.5	253	A53968	serine proteinase
2	563.5	41.2	260	I56559	neuropsin - mouse
3	524	38.3	261	S45303	tissue kallikrein
4	515	37.6	244	A44284	tissue kallikrein
5	510.5	37.3	248	S55066	trypsin (EC 3.4.21)
6	509	37.2	261	1 NGMSG	7S nerve growth fa
7	507	37.0	261	A34079	tissue kallikrein
8	506	37.0	247	A27547	trypsin (EC 3.4.21)
9	506	37.0	261	S01971	tissue kallikrein
10	503	36.7	261	JE0236	tissue kallikrein
11	503	36.7	261	A31136	tissue kallikrein
12	502.5	36.7	246	JQ1472	trypsin (EC 3.4.21)
13	502.5	36.7	261	A29586	tissue kallikrein
14	502	36.7	261	A41020	tissue kallikrein
15	501.5	36.6	250	T01779	trypsin (EC 3.4.21)
16	499.5	36.5	246	1 TRDC	trypsin (EC 3.4.21)
17	498	36.4	261	A32297	semenogelase (EC 3
18	497	36.3	247	S05494	trypsin (EC 3.4.21)
19	497	36.3	259	B31136	tissue kallikrein
20	496	36.2	248	S55067	trypsin (EC 3.4.21)
21	496	36.2	259	A29746	tissue kallikrein
22	496	36.2	265	1 KQRTP	tissue kallikrein
23	495.5	36.2	246	JQ1471	trypsin (EC 3.4.21)
24	492.5	36.0	261	A29745	tissue kallikrein
25	492	35.9	257	S33772	tissue kallikrein
26	491	35.9	261	1 EGMSB	tissue kallikrein
27	488.5	35.7	261	A25606	tissue kallikrein
28	487.5	35.6	262	1 KQHU	tissue kallikrein
29	485	35.4	246	1 TRRT1	trypsin (EC 3.4.21)

30	485	35.4	261	1 S35711	semenogelase (EC 3
31	484	35.4	259	1 KQRTTN	tonin (EC 3.4.21.-
32	484	35.4	261	1 TRMSM5	tissue kallikrein
33	480	35.1	247	2 S13813	trypsin (EC 3.4.21
34	480	35.1	261	1 KQMS1	tissue kallikrein
35	479.5	35.0	229	1 TRBOTR	trypsin (EC 3.4.21
36	479	35.0	246	2 B25528	trypsin (EC 3.4.21
37	476.5	34.8	242	2 S49489	trypsin (EC 3.4.21
38	472.5	34.5	231	1 TRPGTR	trypsin (EC 3.4.21
39	472.5	34.5	247	1 TRDG	trypsin (EC 3.4.21
40	471	34.4	259	2 D23863	tissue kallikrein
41	470.5	34.4	263	2 S15686	tissue kallikrein
42	470	34.3	243	2 A35871	trypsin (EC 3.4.21
43	469.5	34.3	260	2 A37938	tissue kallikrein
44	467.5	34.1	238	2 S31779	trypsin (EC 3.4.21
45	467.5	34.1	247	1 A25852	trypsin (EC 3.4.21

ALIGNMENTS

RESULT 1

A53968
serine proteinase SCCE precursor - human
N:Alternate names: stratum corneum chymotryptic enzyme
C:Species: Homo sapiens (man)
C>Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C:Accession: A53968
R:Hansson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlsteins, A.; Egelrud, T.
J. Biol. Chem. 269, 19420-19426, 1994
A:Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzy
M:Reference number: A53968; MUID:94308225; PMID:8034709
A:Accession: A53968
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-253 <HAN>
A:Cross-references: UNIPROT:P49862; GB:L33404; NID:9521214; PIDN:AAC37551.1; PID:953250
C:Genetics:
A:Gene: GDB:PRSS6; SCCE
A:Map position: 7q35-7q35
A:Superfamily: trypsin; trypsin homology
F:30-245/Domain: trypsin homology <PRI>

Query Match	41.5%;	Score	567.5;	DB 2;	Length	253;			
Best Local Similarity	46.2%;	Pred. No.	1.7e-41;						
Matches	111;	Conservative	40;	Mismatches	82;	Indels	7;	Gaps	4;
y	15	LILGVAGSLVSGSCQIINGEDCSPHSQPWQAAVLWVNEFLFCGVLVHPQWVLSAAHCFQ	74						
b	16	LALETAGEAQG--DKIIDGAPCARGSHPWQVALLSGNLHCGVLNERWVLTAAHCKM	73						
y	75	NSYITGLGHSLEADQEPGSCQVVEASLSVRHPEYRPLLANDMLIKLDESSESDETIRS	134						
b	74	NEYTVHLGSDTL-GDRL--AQRIKASKSRHFGYSTQTHVNDMLVKNLSQARLSMWVK	130						
y	135	ISIASQCPTAGNSCLVSGWGLIANG--RMPTVLQCVNVSVEEVCCKSLYDPLYPHSMFC	192						
b	131	VLPRLSRCEPPGTCTVSGWGTTSPTVFPDMLCDVVKLISPDQCTKYVKDLLENMLC	190						
y	193	AGGGQDQKDSNGDSGGPLICNGYLGVSFGKAPCGQVGVVYTNLCRFTWEIKTVQ	252						
b	191	AGIPDSKKACNGDSGGPLVCRGTLLQGLVSWGTFFCGQPNDRPGVYTVQVCKFTKWINDMK	250						

RESULT 2

I56559
neuropsin - mouse
C:Species: Mus musculus (house mouse)
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: I56559
R:Chen, Z.L.; Yoshida, S.; Kato, K.; Momota, Y.; Suzuki, J.; Tanaka, T.; Ito, J.; Nishik
J. Neurosci. 15, 5088-5097, 1995

A>Title: Expression and activity-dependent changes of a novel limbic-serine protease gen
A;Reference number: I56559; MUID:95348817; PMID:7623137
A;Accession: I56559
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-260 <RES>
A;Cross-references: UNIPROT:O61955; GB:D30785; NID:g1648847; PIDN:BAA06451.1; PID:g10200
C;Superfamily: trypsin; trypsin homology
F;33-252/Domain: trypsin homology <TRY>

Query Match 41.2%; Score 563.5; DB 2; Length 260;
Best Local Similarity 41.3%; Pred. No. 3.8e-41;
Matches 102; Conservative 47; Mismatches 91; Indels 7; Gaps 4;
QY 10 WFLGVLLVAGSLVSGSCQIINGEDCSPHSQPQWQAALVMENELFCGVLVHPQWLSA 69
DB 12 WLLLLFWAGAGLFAQGSKILEGECIPHSQPQWQAALFQGERLICGVLVGDRLVLA 71
QY 70 AHCFQNSYITIGLHLSLEADQEPGQMVESASLVVRHPEYNRPL---LANDMLIKLDES 126
DB 72 AHCKKQKYSVRLGDHSLQSRDQ-EEIQVAQSIQHPCYNNSPEDSHDMLRLQNSA 130
QY 127 SSSDTRISISASQCTAGNSCLVSGWGLLANGR--MPTVLCVNVSVSEVCSKLDP 184
DB 131 NLGDVKVPQLANLCPKVGKQCIISGWTGTPQENFNTLNCAEVKIYSQNKCEAYPG 190
QY 185 LVHPSMFCAAGGQDQKDSGNGSGGPLICNGYLGVSFGKAPCGQGVPGVYTNLCKFT 244
DB 191 KITEGMVCA-GSGNGADTCQGSGLVCDGLQITSGSDPCPKPEKPGVYTKICRYT 249
QY 245 EWIEKTV 251
DB 250 TWIKKT 256

RESULT 3
S45303
tissue kallikrein (EC 3.4.21.35) precursor - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 20-Oct-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: S45303; S38487
R;Gauthier, E.R.; Dumas, C.; Chadelain, P.; Tremblay, R.R.; Dube, J.Y.
Biochim. Biophys. Acta 1218, 102-104, 1994
A;Title: Characterization of canine pancreas kallikrein cDNA.
A;Reference number: S45303; MUID:94250683; PMID:8193155
A;Accession: S45303
A;Molecule type: mRNA
A;Residues: 1-261 <GAU>
A;Cross-references: UNIPROT:Q29474; EMBL:X75479; NID:g414018; PIDN:CAA53210.1; PID:g4140
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase
F;1-24/Domain: signal sequence
F;25-261/Product: tissue kallikrein #status predicted <SIG>
F;25-253/Domain: trypsin homology <TRY>
F;165,120,213/Active site: His, Asp, Ser #status predicted

Query Match 38.3%; Score 524; DB 2; Length 261;
Best Local Similarity 40.3%; Pred. No. 9.7e-38;
Matches 106; Conservative 51; Mismatches 84; Indels 22; Gaps 6;
QY 10 WFLGY-LILVAGSLVSGSC-----SQIINGEDCSPHSQPQWQAALVMENELFCGVLVHPQ 64
DB 2 WFLVCLALSLAG---TGAAPVPVSRIGGWDCTKNSQPWQAALVHYSKFCQGGVLVHPE 58
QY 65 WYLSAHCFSQSYITIGLHLSLEADQEPGQMVESASLVVRHPEYNRPLAN----- 115
DB 59 WYVTAACINDNYQLWGRYNL-FHEDTAQPVQVRESFPFPEFNLKHLKHLRPLEEDY 117
QY 116 -DMLMLIKLDESVDTRISIASQCTAGNSCLVSGWGLLANGRM--PTVLCVNVSV 171
DB 118 SHDMLRLAEPQAQITDAVRVLDLTQEPVGSTCYAGWSGSIKPKFIYDDQLQCVLDLE 177
QY 172 VVSEVCSKLVDPLVHPSMFCAGGQDQKDSGNGSGGPLICNGYLGVSFGKAPCGQV 231

Db 178 LLSNDICANAHSQKVTEFMLCAGHLEGCKDTGVSGGPLICDGVLOGITSGHGVPCGSP 237
QY 232 GVPGVYTNLCKFTETWIKTVQAS 254
DB 238 NMPAVYTKVISHLEWIKETMTAN 260
RESULT 4
A44284
tissue kallikrein (EC 3.4.21.35) homolog - rat (fragment)
N;Alternate names: proteinase B light chain
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A44284; C41429
R;Ma, J.X.; Chao, J.; Chao, L., 1992
Biochemistry 31, 10922-10928, 1992
A;Title: Molecular cloning and characterization of rKlk10, a cDNA encoding T-kininogenas
A;Reference number: A44284; MUID:93041794; PMID:1420203
A;Accession: A44284
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-244 <MAL>
A;Cross-references: UNIPROT:P36375; GB:S48142; NID:g259430; PIDN:AAB24071.1; PID:g259431
A;Experimental source: submandibular gland
A;Note: sequence extracted from NCBI backbone (NCBI:118095, NCBI:118096)
R;Kato, H.; Nakanishi, E.; Enjiyoji, K.; Hayashi, I.; Oh-Iehi, S.; Iwanaga, S.
J. Biochem. 102, 1389-1404, 1987
A;Title: Characterization of serine proteinases isolated from rat submaxillary gland: wi
A;Reference number: A41429; MUID:88198057; PMID:3482210
A;Accession: C41429
A;Status: preliminary
A;Molecule type: protein
A;Residues: 10-61 <KAT>
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase
F;10-236/Domain: trypsin homology <TRY>
F;48,103,196/Active site: His, Asp, Ser #status predicted

Query Match 37.6%; Score 515; DB 2; Length 244;
Best Local Similarity 42.4%; Pred. No. 5.3e-37;
Matches 101; Conservative 42; Mismatches 77; Indels 18; Gaps 5;
QY 29 SQIINGEDCSPHSQPQWQAALVMENELFCGVLVHPQWLSAACHFQNSYITIGLHLSLEA 88
DB 8 SRIVGVYKCKNSQPVQVAIL--NEYLGGVLIIDPSWVITAAHCYSNYHYHLLGNLPE 65
QY 89 DQEPGQMVESASLVVRHPEYNRPL-----ANDMLIKLDESVDTRISIS 136
DB 66 D-EPPAQVRFVNVQSFPHPDY-KPFLMRNHTRQRGDYSNDLMLLHLSBPADITDGVKVID 123
QY 137 IASQCPAGNSCLVSGWGLL--ANGRMPTVLCVNVSVSEVCSKLVDPLVHPSMFCAG 194
DB 124 LPTBEPKVGSTCLASGWSGKPLNWEPLDDIQQCNHLLSNEKCIETAEYEQKVTDLMLCAG 183
QY 195 GGQDQKDSGNGSGGPLICNGYLGVSFGKAPCGQGVPGVYTNLCKFTETWIKTVQ 252
DB 184 EMDGRKTCRKGDSGGPLICDGVLOGITSGWNVPCAEPVNVYTKLIKFTSWIKVMK 241

RESULT 5
S55066
trypsin (EC 3.4.21.4) II precursor, pancreatic (clone 2-P29) - chicken
N;Alternate names: trypsinogen II
C;Species: Gallus gallus (chicken)
C;Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: S55066; S72347
R;Wang, K.; Gan, L.; Lee, I.; Hood, L.
Biochem. J. 307, 471-479, 1995
A;Title: Isolation and characterization of the chicken trypsinogen gene family.
A;Reference number: S55065; MUID:95251611; PMID:7733885
A;Accession: S55066
A;Molecule type: mRNA

J. Biol. Chem. 256, 9156-9166, 1981

A;Title: The amino acid sequence of the gamma-subunit of mouse submaxillary gland 7 S rN

A;Reference number: A92341; MUID:81264363; PMID:7263706

A;Accession: A92341

A:Molecule type: protein

A;Residues: 25-107,112-261 <THO>

A;Experimental source: outbred strain Swiss Webster

C;Comment: 7S nerve growth factor is composed of two alpha chains, a beta dimer compose

C;Comment: The active form of the gamma chain occurs naturally as combinations of eithe

C;Genetics:

A;Map position: 7

A;Introns: 16/1; 69/2; 165/1; 210/3

C;Superfamily: trypsin; trypsin homology

C;Keywords: glycoprotein; growth factor; hydrolase; serine proteinase; submandibular gl

F;1-18/Domain: signal sequence #status predicted <SIG>

F;25-253/Domain: trypsin homology <TRY>

F;25-107/Domain: segment B1 <GB1>

F;25-107,112-261/Product: nerve growth factor gamma chain (active form) #status experim

F;112-261/Domain: segment A <GAA>

F;112-164/Domain: segment C <GCC>

F;165-261/Domain: segment B2 <GB2>

F;31-173,50-66,152-219,184-198,209-234/Disulfide bonds: #status predicted

F;65,120,213/Active site: His, Asp, Ser #status predicted

F;102/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 37.2%; Score 509; DB 1; Length 261;
Best Local Similarity 39.5%; Pred. No.1.9e-36;
Matches 103; Conservative 48; Mismatches 86; Indels 24; Gaps 6;

QY 10 WFL-GVLIIGVAG-SLVSGSCQINGEDCSPHSQPQAALVMENELFCSGVLVHPQWVL 67
||| ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 2 WFLFLFSLSLGIDGAAPPVQSRIVGFGFKCNKSPHWAVRYRTQYLCGGVLLDPNWVL 61
||| ||| : : : : : : : : : : : : : : : : : : : : : : : :

QY 68 SAHCFQNSYTICGLHSLEADQEGCSOMVEASLSVRHPEYNRPLL-----AND 116
: ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 62 TTAHCYDDNKVWLGNKNLFKD-BPSAQHRFVSKAIPHGFNMSLMRKHIRFLEYDYSND 120
||| ||| : : : : : : : : : : : : : : : : : : : : : : : :

QY 117 LMLIKLDESVSRSDTIRSISASQCPTAGNSCLVSGWGLLANGRMPTVLQ-----CVNV 170
: ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 LMLRLSKPADITDVTKPIPLTEBPKLGSTCLASGWGSIT---PTKFQTDLDLCVNL 176
||| ||| : : : : : : : : : : : : : : : : : : : : : : : :

QY 171 SVSVBVCVKLYDPLVHPFMFCAGGQQDKDCNGDSGGPLICNGYLGVSPGKAPCGQ 230
||| ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 177 KLLPNEDCAKAHEKVETDAMLCAGEDMGKGDKTCGDSGGPLICDGLVQLGTWSGHTPCGE 236
||| ||| : : : : : : : : : : : : : : : : : : : : : : : :

QY 231 VGVPGVVYTNLCKFTFEWIEKTIV 251
: ||| ||| ||| ||| ||| : : : : : : : : : : : : : : : : :
Db 237 PDMPGVVYTNLKPKFTSWIKDTM 257
: ||| ||| ||| ||| ||| : : : : : : : : : : : : : : : : :

RESULT 7

A34079

tissue kallikrein (EC 3.4.21.35) P1 precursor - rat

N;Alternate names: kallikrein-related proteinase k8

C;Species: Rattus norvegicus (Norway rat)

C;Date: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 09-Jul-2004

C;Accession: A34079; S10700

R;Brady, J.M.; Wines, D.R.; MacDonald, R.J.

Biochemistry 28, 5203-5210, 1989

A;Title: Expression of two kallikrein gene family members in the rat prostate.

A;Reference number: A34079; MUID:89352606; PMID:2765531

A;Accession: A34079

A>Status: preliminary

A:Molecule type: DNA; mRNA

A;Residues: 1-261 <BRA>

A;Cross-references: UNIPROT:P36374; GB:M27215; GB:M27216; GB:M27217; NID:g206638; PIDN:

A;Experimental source: prostate

R;Elmoujahed, A.; Gutman, N.; Brillard, M.; Gauthier, F.

FEBS Lett. 265, 137-140, 1990

A;Title: Substrate specificity of two kallikrein family gene products isolated from the

A;Reference number: S10698; MUID:90306305; PMID:2194829

A;Accession: S10700

A:Molecule type: protein

A:Molecule type: mRNA
A:Residues: 1-250 <LEA>
A:Cross-references: EMBL:X56744; NID:g1213630; PID:g64240
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; protein digestion; serine proteinase
F:23-242/Domain: trypsin homology <TRY>

Query Match 36.6%; Score 501.5; DB 2; Length 250;
Best Local Similarity 42.3%; Pred. No. 8e-36;
Matches 105; Conservative 37; Mismatches 97; Indels 9; Gaps 5;

QY	12	LGVLILGVAGSLVSGSQIINGEDCSPHSQPWQAALVMENELFCSGVLVHPQWVLSAAH	71
DB	4	LALLLVGAAVAVPREDGRIIGHECAHSRPFMASLNYGYH-FCGGVLINQWVLSVAH	62
QY	72	CFQNSYT--IGLGLHSLDAQEPGSQWVEASLSVRHPEYNRPRLANDLMLIKLDESVSSES	129
DB	63	CWYNPVAMQVMLGEHDLR-KFEGTEQLMKTTDTIIWHPNYDYQTLDFDIMLIKLYHPVEVS	121
QY	130	DTIRISIASQCPTAGNSCLVSGWLLANG----RMPTVLQCVNVSVSEVCSKLYDPL	185
DB	122	HAYGPIPLTSCPVAGTSCVSGWNTARDGDEVYLTLLQCMDFIVDDEEQCMKSYDPM	181
QY	186	YHPSMFCAGGQDQKDSNGDSGGPLICNGYLOGLYSFGKAPCGGVGVVYTNLCKFTE	245
DB	182	ISPRMVCAGFMDSRDACNGDSGLVCRGEVYGLVSWGQG-CAQPNYPGVVYVYKLCEFLG	240
QY	246	WIEKTVQA 253	
DB	241	WIERLEA 248	

Search completed: February 10, 2005, 08:55:01
Job time : 41 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2005, 08:54:22 ; Search time 128 Seconds
(without alignments)
648.393 Million cell updates/sec

Title: US-09-895-814-525
Perfect score: 1369
Sequence: 1 MATAGNPMGWFGLYLGLVA.....GVYTNLCCKFTWIEKTVQAS 254

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues
Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1369	100.0	254	9 US-09-759-143-525	Sequence 525, App
2	1369	100.0	254	9 US-09-780-669-525	Sequence 525, App
3	1369	100.0	254	9 US-09-822-827-525	Sequence 525, App
4	1369	100.0	254	9 US-09-895-793-525	Sequence 525, App
5	1369	100.0	254	9 US-09-895-814-525	Sequence 525, App
6	1369	100.0	254	13 US-10-012-896-525	Sequence 525, App
7	1369	100.0	254	14 US-10-010-940-525	Sequence 525, App
8	1369	100.0	254	14 US-10-144-678A-525	Sequence 525, App
9	1369	100.0	254	14 US-10-294-025-525	Sequence 525, App
10	1369	100.0	254	16 US-10-473-485-6	Sequence 525, App
11	1369	100.0	254	16 US-10-473-485-13	Sequence 525, App
12	1369	100.0	1079	9 US-09-822-827-947	Sequence 947, App
13	1369	100.0	1079	9 US-09-895-793-947	Sequence 947, App

14	1364	99.6	254	14	US-10-312-089-7	Sequence 7, Appli
15	1352	98.8	254	9	US-09-759-143-523	Sequence 523, App
16	1352	98.8	254	9	US-09-780-669-523	Sequence 523, App
17	1352	98.8	254	9	US-09-822-827-523	Sequence 523, App
18	1352	98.8	254	9	US-09-895-793-523	Sequence 523, App
19	1352	98.8	254	9	US-09-895-814-523	Sequence 523, App
20	1352	98.8	254	13	US-10-012-896-523	Sequence 523, App
21	1352	98.8	254	14	US-10-010-940-523	Sequence 523, App
22	1352	98.8	254	14	US-10-144-678A-523	Sequence 523, App
23	1352	98.8	254	14	US-10-294-025-523	Sequence 523, App
24	1348.5	98.5	253	15	US-10-344-334-37	Sequence 37, Appli
25	1205	88.0	449	9	US-09-759-143-617	Sequence 617, App
26	1205	88.0	449	9	US-09-780-669-617	Sequence 617, App
27	1205	88.0	449	9	US-09-822-827-617	Sequence 617, App
28	1205	88.0	449	9	US-09-895-793-617	Sequence 617, App
29	1205	88.0	449	9	US-09-895-814-617	Sequence 617, App
30	1205	88.0	449	13	US-10-012-896-617	Sequence 617, App
31	1205	88.0	449	14	US-10-144-678A-617	Sequence 617, App
32	1205	88.0	449	14	US-10-294-025-617	Sequence 617, App
33	1205	88.0	585	9	US-09-822-827-978	Sequence 978, App
34	1205	88.0	585	9	US-09-822-827-981	Sequence 981, App
35	1205	88.0	585	9	US-09-895-793-978	Sequence 978, App
36	1205	88.0	585	9	US-09-895-793-981	Sequence 981, App
37	1205	88.0	585	14	US-10-144-678A-1020	Sequence 1020, Ap
38	1205	88.0	585	14	US-10-294-025-1020	Sequence 1020, Ap
39	1205	88.0	801	9	US-09-822-827-982	Sequence 982, App
40	1205	88.0	801	9	US-09-895-793-982	Sequence 982, App
41	1191	87.0	226	14	US-10-312-089-8	Sequence 8, Appli
42	1191	87.0	312	14	US-10-312-089-3	Sequence 3, Appli
43	1191	87.0	344	9	US-09-822-827-973	Sequence 973, App
44	1191	87.0	344	9	US-09-895-793-973	Sequence 973, App
45	1185	86.6	220	9	US-09-759-143-327	Sequence 327, App

ALIGNMENTS

RESULT 1
US-09-759-143-525
; Sequence 525, Application US/09759143
; Patent No. US20020022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillion, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 525
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-759-143-525
Query Match 100.0%; Score 1369; DB 9; Length 254;

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Best Local Similarity 100.0%; Pred. No. 1.3e-129;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATAGNPGWFLGYLLILGVAGSLVSGSCQIINGEDCSPHSQPWOAALVMENELFCSGVL 60
Db 1 MATAGNPGWFLGYLLILGVAGSLVSGSCQIINGEDCSPHSQPWOAALVMENELFCSGVL 60
QY 61 VHPQWLSAAHCFQNSYTTIGLHLSLEADQEPGSMVEASLSVRHPEYNRPLLANDMLI 120
Db 61 VHPQWLSAAHCFQNSYTTIGLHLSLEADQEPGSMVEASLSVRHPEYNRPLLANDMLI 120
QY 121 KLDESVSSEDTRISISIAQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
Db 121 KLDESVSSEDTRISISIAQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
QY 181 LYDPLYHPMFAGGQDQKDCSCNGDSGGPLICNGYLGSLVFGKAPCGQGVPGVYTNL 240
Db 181 LYDPLYHPMFAGGQDQKDCSCNGDSGGPLICNGYLGSLVFGKAPCGQGVPGVYTNL 240
QY 241 CKFTWIEKTVQAS 254
Db 241 CKFTWIEKTVQAS 254

RESULT 2
US-09-780-669-525
; Sequence 525, Application US/09780669
; Patent No. US2002005197A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Kallós, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 525
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-780-669-525

Query Match 100.0%; Score 1369; DB 9; Length 254;
Best Local Similarity 100.0%; Pred. No. 1.3e-129;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATAGNPGWFLGYLLILGVAGSLVSGSCQIINGEDCSPHSQPWOAALVMENELFCSGVL 60
Db 1 MATAGNPGWFLGYLLILGVAGSLVSGSCQIINGEDCSPHSQPWOAALVMENELFCSGVL 60
QY 61 VHPQWLSAAHCFQNSYTTIGLHLSLEADQEPGSMVEASLSVRHPEYNRPLLANDMLI 120
Db 61 VHPQWLSAAHCFQNSYTTIGLHLSLEADQEPGSMVEASLSVRHPEYNRPLLANDMLI 120
QY 121 KLDESVSSEDTRISISIAQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
Db 121 KLDESVSSEDTRISISIAQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
QY 181 LYDPLYHPMFAGGQDQKDCSCNGDSGGPLICNGYLGSLVFGKAPCGQGVPGVYTNL 240
Db 181 LYDPLYHPMFAGGQDQKDCSCNGDSGGPLICNGYLGSLVFGKAPCGQGVPGVYTNL 240
QY 241 CKFTWIEKTVQAS 254
Db 241 CKFTWIEKTVQAS 254

RESULT 3
US-09-822-827-525
; Sequence 525, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 525
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-822-827-525

Query Match 100.0%; Score 1369; DB 9; Length 254;
Best Local Similarity 100.0%; Pred. No. 1.3e-129;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATAGNPGWFLGYLLILGVAGSLVSGSCQIINGEDCSPHSQPWOAALVMENELFCSGVL 60
Db 1 MATAGNPGWFLGYLLILGVAGSLVSGSCQIINGEDCSPHSQPWOAALVMENELFCSGVL 60
QY 61 VHPQWLSAAHCFQNSYTTIGLHLSLEADQEPGSMVEASLSVRHPEYNRPLLANDMLI 120
Db 61 VHPQWLSAAHCFQNSYTTIGLHLSLEADQEPGSMVEASLSVRHPEYNRPLLANDMLI 120
QY 121 KLDESVSSEDTRISISIAQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
Db 121 KLDESVSSEDTRISISIAQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
QY 181 LYDPLYHPMFAGGQDQKDCSCNGDSGGPLICNGYLGSLVFGKAPCGQGVPGVYTNL 240
Db 181 LYDPLYHPMFAGGQDQKDCSCNGDSGGPLICNGYLGSLVFGKAPCGQGVPGVYTNL 240
QY 241 CKFTWIEKTVQAS 254
Db 241 CKFTWIEKTVQAS 254

RESULT 4
US-09-895-793-525
; Sequence 525, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Kallós, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
```

```

; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 525
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-895-793-525

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Query Match      100.0%; Score 1369; DB 9; Length 254;
Best Local Similarity 100.0%; Pred. No. 1.3e-129;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MATAGNPGWFLGYLLGVAGSLVSGSCSQIINGEDCSPHSQPWQAALVMENELFCSGVL 60
DB 1 MATAGNPGWFLGYLLGVAGSLVSGSCSQIINGEDCSPHSQPWQAALVMENELFCSGVL 60
QY 61 VHPQWLSAAHCFQNSYTTIGLGLHSLADQEPGQSMVEASLSVRHPEYNRPILLANDMLI 120
DB 61 VHPQWLSAAHCFQNSYTTIGLGLHSLADQEPGQSMVEASLSVRHPEYNRPILLANDMLI 120
QY 121 KLDESVSDDTIRSIASQCTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
DB 121 KLDESVSDDTIRSIASQCTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
QY 181 LYDPLVHPSMFCAGGQDQKSCNGDSGGPLICNGYLOGLVSGKAPCGQGVPGVYTNL 240
DB 181 LYDPLVHPSMFCAGGQDQKSCNGDSGGPLICNGYLOGLVSGKAPCGQGVPGVYTNL 240
QY 241 CKFTWIEKTVQAS 254
DB 241 CKFTWIEKTVQAS 254

```

RESULT 5

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US-09-895-814-525
; Sequence 525, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.

```

```

; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 525
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-895-814-525

```

```

Query Match      100.0%; Score 1369; DB 9; Length 254;
Best Local Similarity 100.0%; Pred. No. 1.3e-129;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MATAGNPGWFLGYLLGVAGSLVSGSCSQIINGEDCSPHSQPWQAALVMENELFCSGVL 60
DB 1 MATAGNPGWFLGYLLGVAGSLVSGSCSQIINGEDCSPHSQPWQAALVMENELFCSGVL 60
QY 61 VHPQWLSAAHCFQNSYTTIGLGLHSLADQEPGQSMVEASLSVRHPEYNRPILLANDMLI 120
DB 61 VHPQWLSAAHCFQNSYTTIGLGLHSLADQEPGQSMVEASLSVRHPEYNRPILLANDMLI 120
QY 121 KLDESVSDDTIRSIASQCTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
DB 121 KLDESVSDDTIRSIASQCTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
QY 181 LYDPLVHPSMFCAGGQDQKSCNGDSGGPLICNGYLOGLVSGKAPCGQGVPGVYTNL 240
DB 181 LYDPLVHPSMFCAGGQDQKSCNGDSGGPLICNGYLOGLVSGKAPCGQGVPGVYTNL 240
QY 241 CKFTWIEKTVQAS 254
DB 241 CKFTWIEKTVQAS 254

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RESULT 6

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US-10-012-896-525
; Sequence 525, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 525
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-895-814-525

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; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 525
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-896-525

Query Match      100.0%; Score 1369; DB 13; Length 254;
Best Local Similarity 100.0%; Pred. No. 1.3e-129;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATAGNPWGFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWQAALVMENELFCSGVL 60
Db 1 MATAGNPWGFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWQAALVMENELFCSGVL 60

QY 61 VHPQWLSAAHCFQNSYITIGLHLSLEADQEPGSMVEASLSVRHPEYNRPILLANDMLI 120
Db 61 VHPQWLSAAHCFQNSYITIGLHLSLEADQEPGSMVEASLSVRHPEYNRPILLANDMLI 120

QY 121 KLDSESVESDTRISISASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
Db 121 KLDSESVESDTRISISASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180

QY 181 LYDPLYPHSMFCAGGQDQKSCNGDSGGPLICNGYLGVSFGKAPCGQGVPGVYTNL 240
Db 181 LYDPLYPHSMFCAGGQDQKSCNGDSGGPLICNGYLGVSFGKAPCGQGVPGVYTNL 240

QY 241 CKFTEWIEKTVQAS 254
Db 241 CKFTEWIEKTVQAS 254

RESULT 8
US-10-144-678A-525
; Sequence 525, Application US/10144678A
; Publication No. US20030157089A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C28
; CURRENT APPLICATION NUMBER: US/10/144,678A
; CURRENT FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 525
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-678A-525

Query Match      100.0%; Score 1369; DB 14; Length 254;
Best Local Similarity 100.0%; Pred. No. 1.3e-129;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATAGNPWGFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWQAALVMENELFCSGVL 60
Db 1 MATAGNPWGFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWQAALVMENELFCSGVL 60

QY 61 VHPQWLSAAHCFQNSYITIGLHLSLEADQEPGSMVEASLSVRHPEYNRPILLANDMLI 120
Db 61 VHPQWLSAAHCFQNSYITIGLHLSLEADQEPGSMVEASLSVRHPEYNRPILLANDMLI 120

QY 121 KLDSESVESDTRISISASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
Db 121 KLDSESVESDTRISISASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180

QY 181 LYDPLYPHSMFCAGGQDQKSCNGDSGGPLICNGYLGVSFGKAPCGQGVPGVYTNL 240
Db 181 LYDPLYPHSMFCAGGQDQKSCNGDSGGPLICNGYLGVSFGKAPCGQGVPGVYTNL 240

QY 241 CKFTEWIEKTVQAS 254
Db 241 CKFTEWIEKTVQAS 254

RESULT 7
US-10-010-940-525
; Sequence 525, Application US/10010940
; Publication No. US2003008062A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqiu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427D3
; CURRENT APPLICATION NUMBER: US/10/010,940
; CURRENT FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 525
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-010-940-525

Query Match      100.0%; Score 1369; DB 14; Length 254;
Best Local Similarity 100.0%; Pred. No. 1.3e-129;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATAGNPWGFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWQAALVMENELFCSGVL 60
Db 1 MATAGNPWGFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWQAALVMENELFCSGVL 60
```

Db 121 KLDSESVESDTRISIASQCPTAGNSCLVSGHGLLANGRMPTVLQCVNVSVSEVCSK 180
Qy 181 LYDPLYPHSMFCAGGQDQKDCNSGDSGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
Db 181 LYDPLYPHSMFCAGGQDQKDCNSGDSGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
Qy 241 CKFTWIEKTVQAS 254
Db 241 CKFTWIEKTVQAS 254

RESULT 9

US-10-294-025-525

; Sequence 525, Application US/10294025

; Publication No. US20030185830A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Stolk, John A.

; APPLICANT: Kalos, Michael D.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.427C29

; CURRENT APPLICATION NUMBER: US/10/294,025

; CURRENT FILING DATE: 2002-11-12

; NUMBER OF SEQ ID NOS: 1038

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 525

; LENGTH: 254

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-294-025-525

Query Match 100.0%; Score 1369; DB 14; Length 254;
Best Local Similarity 100.0%; Pred. No. 1.3e-129;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATAGNPMGWFLGYLLILGVAGSLVSGSCSQIINGEDCSPHSQPWOAALVWENELFCSGVL 60
Db 1 MATAGNPMGWFLGYLLILGVAGSLVSGSCSQIINGEDCSPHSQPWOAALVWENELFCSGVL 60
Qy 61 VHPQWVLSAAHCFQNSYTTIGLHLSLEADQEPGSMVEASLSVRHPEYRPLLANDMLI 120
Db 61 VHPQWVLSAAHCFQNSYTTIGLHLSLEADQEPGSMVEASLSVRHPEYRPLLANDMLI 120
Qy 121 KLDSESVESDTRISIASQCPTAGNSCLVSGHGLLANGRMPTVLQCVNVSVSEVCSK 180
Db 121 KLDSESVESDTRISIASQCPTAGNSCLVSGHGLLANGRMPTVLQCVNVSVSEVCSK 180
Qy 181 LYDPLYPHSMFCAGGQDQKDCNSGDSGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
Db 181 LYDPLYPHSMFCAGGQDQKDCNSGDSGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
Qy 241 CKFTWIEKTVQAS 254
Db 241 CKFTWIEKTVQAS 254

RESULT 10

US-10-473-485-6

; Sequence 6, Application US/10473485

; Publication No. US20040137455A1

; GENERAL INFORMATION:

; APPLICANT: Clements, Judith A

; APPLICANT: Dong, Ying

; TITLE OF INVENTION: Polynucleotides and polypeptides linked to cancer and/or benign

; FILE REFERENCE: DAV1172.004APC

; CURRENT APPLICATION NUMBER: US/10/473,485

; CURRENT FILING DATE: 2003-09-29

; PRIOR APPLICATION NUMBER: AU PR4022/01

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 6

; LENGTH: 254
; TYPE: PRT
; ORGANISM: human
US-10-473-485-6

Query Match 100.0%; Score 1369; DB 16; Length 254;
Best Local Similarity 100.0%; Pred. No. 1.3e-129;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATAGNPMGWFLGYLLILGVAGSLVSGSCSQIINGEDCSPHSQPWOAALVWENELFCSGVL 60
Db 1 MATAGNPMGWFLGYLLILGVAGSLVSGSCSQIINGEDCSPHSQPWOAALVWENELFCSGVL 60
Qy 61 VHPQWVLSAAHCFQNSYTTIGLHLSLEADQEPGSMVEASLSVRHPEYRPLLANDMLI 120
Db 61 VHPQWVLSAAHCFQNSYTTIGLHLSLEADQEPGSMVEASLSVRHPEYRPLLANDMLI 120
Qy 121 KLDSESVESDTRISIASQCPTAGNSCLVSGHGLLANGRMPTVLQCVNVSVSEVCSK 180
Db 121 KLDSESVESDTRISIASQCPTAGNSCLVSGHGLLANGRMPTVLQCVNVSVSEVCSK 180
Qy 181 LYDPLYPHSMFCAGGQDQKDCNSGDSGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
Db 181 LYDPLYPHSMFCAGGQDQKDCNSGDSGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
Qy 241 CKFTWIEKTVQAS 254
Db 241 CKFTWIEKTVQAS 254

RESULT 11

US-10-473-485-13

; Sequence 13, Application US/10473485

; Publication No. US20040137455A1

; GENERAL INFORMATION:

; APPLICANT: Clements, Judith A

; APPLICANT: Dong, Ying

; TITLE OF INVENTION: Polynucleotides and polypeptides linked to cancer and/or benign

; FILE REFERENCE: DAV1172.004APC

; CURRENT APPLICATION NUMBER: US/10/473,485

; CURRENT FILING DATE: 2003-09-29

; PRIOR APPLICATION NUMBER: AU PR4022/01

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 13

; LENGTH: 254

; TYPE: PRT

; ORGANISM: human

US-10-473-485-13

Query Match 100.0%; Score 1369; DB 16; Length 254;
Best Local Similarity 100.0%; Pred. No. 1.3e-129;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATAGNPMGWFLGYLLILGVAGSLVSGSCSQIINGEDCSPHSQPWOAALVWENELFCSGVL 60
Db 1 MATAGNPMGWFLGYLLILGVAGSLVSGSCSQIINGEDCSPHSQPWOAALVWENELFCSGVL 60
Qy 61 VHPQWVLSAAHCFQNSYTTIGLHLSLEADQEPGSMVEASLSVRHPEYRPLLANDMLI 120
Db 61 VHPQWVLSAAHCFQNSYTTIGLHLSLEADQEPGSMVEASLSVRHPEYRPLLANDMLI 120
Qy 121 KLDSESVESDTRISIASQCPTAGNSCLVSGHGLLANGRMPTVLQCVNVSVSEVCSK 180
Db 121 KLDSESVESDTRISIASQCPTAGNSCLVSGHGLLANGRMPTVLQCVNVSVSEVCSK 180
Qy 181 LYDPLYPHSMFCAGGQDQKDCNSGDSGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
Db 181 LYDPLYPHSMFCAGGQDQKDCNSGDSGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
Qy 241 CKFTWIEKTVQAS 254
Db 241 CKFTWIEKTVQAS 254

Db 241 CKTEWIEKTVOAS 254

RESULT 12
US-09-822-827-947
; Sequence 947, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 947
; LENGTH: 1079
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-822-827-947

Query Match 100.0%; Score 1369; DB 9; Length 1079;
Best Local Similarity 100.0%; Pred. No. 8.4e-129;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATAGNPMGWFLGYLILGVAGSLVSGSCSIINGEDCSPHSQPWQAALVMENELFCSGVL 60
Db 271 MATAGNPMGWFLGYLILGVAGSLVSGSCSIINGEDCSPHSQPWQAALVMENELFCSGVL 330

QY 61 VHPQWLSAAHCFQNSYTTIGLGLHSLLEADQEPGSMVEASLSVRHPEYNRPRLANDLMLI 120
Db 331 VHPQWLSAAHCFQNSYTTIGLGLHSLLEADQEPGSMVEASLSVRHPEYNRPRLANDLMLI 390

QY 121 KLDESVSSEDDTIRSIASQCTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
Db 391 KLDESVSSEDDTIRSIASQCTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 450

QY 181 LYDPLVHPSMFCAGGQDKSCNGDSGGPLICNGYLQGLVFGKAPCGQGVPGVYTNL 240
Db 451 LYDPLVHPSMFCAGGQDKSCNGDSGGPLICNGYLQGLVFGKAPCGQGVPGVYTNL 510

QY 241 CKTEWIEKTVOAS 254
Db 511 CKTEWIEKTVOAS 524

RESULT 13
US-09-895-793-947
; Sequence 947, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa

; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 947
; LENGTH: 1079
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-895-793-947

Query Match 100.0%; Score 1369; DB 9; Length 1079;
Best Local Similarity 100.0%; Pred. No. 8.4e-129;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATAGNPMGWFLGYLILGVAGSLVSGSCSIINGEDCSPHSQPWQAALVMENELFCSGVL 60
Db 271 MATAGNPMGWFLGYLILGVAGSLVSGSCSIINGEDCSPHSQPWQAALVMENELFCSGVL 330

QY 61 VHPQWLSAAHCFQNSYTTIGLGLHSLLEADQEPGSMVEASLSVRHPEYNRPRLANDLMLI 120
Db 331 VHPQWLSAAHCFQNSYTTIGLGLHSLLEADQEPGSMVEASLSVRHPEYNRPRLANDLMLI 390

QY 121 KLDESVSSEDDTIRSIASQCTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
Db 391 KLDESVSSEDDTIRSIASQCTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 450

QY 181 LYDPLVHPSMFCAGGQDKSCNGDSGGPLICNGYLQGLVFGKAPCGQGVPGVYTNL 240
Db 451 LYDPLVHPSMFCAGGQDKSCNGDSGGPLICNGYLQGLVFGKAPCGQGVPGVYTNL 510

QY 241 CKTEWIEKTVOAS 254
Db 511 CKTEWIEKTVOAS 524

RESULT 14
US-10-312-089-7
; Sequence 7, Application US/10312089
; Publication No. US20030143240A1
; GENERAL INFORMATION:
; APPLICANT: Cabezon-Silva, Teresa Elisa Virginia
; APPLICANT: Permann, Philippe Jean Gervais Ghislain
; TITLE OF INVENTION: Prostate Protein Vaccine Comprising
; TITLE OF INVENTION: Derivatized Thiol Residues and Methods for Producing Said
; TITLE OF INVENTION: Antigen
; FILE REFERENCE: B45224
; CURRENT APPLICATION NUMBER: US/10/312,089
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: PCT/EP01/07082
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: GB 0015722.2
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-312-089-7

Query Match 99.6%; Score 1364; DB 14; Length 254;
Best Local Similarity 99.6%; Pred. No. 4.1e-129;
Matches 253; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATAGNPMGWFLGYLILGVAGSLVSGSCSIINGEDCSPHSQPWQAALVMENELFCSGVL 60
Db 1 MATAGNPMGWFLGYLILGVAGSLVSGSCSIINGEDCSPHSQPWQAALVMENELFCSGVL 60

QY 61 VHPQWLSAAHCFQNSYTTIGLGLHSLLEADQEPGSMVEASLSVRHPEYNRPRLANDLMLI 120

Db 61 VHPQWLSAAHCFQNSYTTIGLHLSLEADQEPGQVMEASLSVRHPEYNRPRLANDMLI 120
QY 121 KLDSESVESDTIRSIASQCPAGNSCLVSGWGLLANGRMPTVLCVNVSVVSEVCSK 180
Db 121 KLDSESVESDTIRSIASQCPAGNSCLVSGWGLLANGRMPTVLCVNVSVVSEVCSK 180
QY 181 LYDPLVHPSMFCAGGQDQKXDCNCGSGGPLICNGYLQGLVSGKAPCGQVGPVYTNL 240
Db 181 LYDPLVHPSMFCAGGHDQKXDCNCGSGGPLICNGYLQGLVSGKAPCGQVGPVYTNL 240
QY 241 CKFTWIEKTVQAS 254
Db 241 CKFTWIEKTVQAS 254

RESULT 15

US-09-759-143-523
; Sequence 523, Application US/09759143
; Patent No. US2002022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 523
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
; NAME/KEY: VARIANT
; LOCATION: (1)...(254)
; OTHER INFORMATION: Xaa = any amino acid
US-09-759-143-523

Query Match 98.8%; Score 1352; DB 9; Length 254;
Best Local Similarity 98.8%; Pred. No. 6.7e-128;
Matches 251; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MATAGNPWGFWFLGYLLGVAGSLVSGSCQIINGEDCSPHSQWPQAAALVMENELFCSGYL 60
Db 1 MATAGNPWGFWFLGYLLGVAGSLVSGSCQIINGEDCSPHSQWPQAAALVMENELFCSGYL 60
QY 61 VHPQWLSAAHCFQNSYTTIGLHLSLEADQEPGQVMEASLSVRHPEYNRPRLANDMLI 120
Db 61 VHPQWLSATHCFQNSYTTIGLHLSLEADQEPGQVMEASLSVRHPEYNRPRLANDMLI 120
QY 121 KLDSESVESDTIRSIASQCPAGNSCLVSGWGLLANGRMPTVLCVNVSVVSEVCSK 180
Db 121 KLDSESVESDTIRSIASQCPAGNSCLVSGWGLLANGRMPTVLCVNVSVVSEVCSK 180
QY 181 LYDPLVHPSMFCAGGQDQKXDCNCGSGGPLICNGYLQGLVSGKAPCGQVGPVYTNL 240

Db 181 LYDPLVHPSMFCAGGQXQXDCNCGSGGPLICNGYLQGLVSGKAPCGQVGPVYTNL 240
QY 241 CKFTWIEKTVQAS 254
Db 241 CKFTWIEKTVQAS 254
Search completed: February 10, 2005, 09:06:41
Job time : 129 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2005, 08:48:01 ; Search time 42 Seconds
(without alignments)
451.449 Million cell updates/sec

Title: US-09-895-814-525
Perfect score: 1369
Sequence: 1 MATAGNPGWFLGYLILGVA.....GVYTNLCKFTETWIKTVQAS 254

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2.6/prodata/1/iaa/5B COMB.pep:*
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4: /cgn2.6/prodata/1/iaa/6B COMB.pep:*
5: /cgn2.6/prodata/1/iaa/PCTUS COMB.pep:*
6: /cgn2.6/prodata/1/iaa/backfile1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1369	100.0	254	3	US-09-439-313-525
2	1369	100.0	254	4	US-09-636-215-525
3	1369	100.0	254	4	US-09-685-166A-525
4	1369	100.0	254	4	US-09-679-426-525
5	1369	100.0	254	4	US-09-759-143-525
6	1369	100.0	254	4	US-09-651-236-525
7	1352	98.8	254	3	US-09-439-313-523
8	1352	98.8	254	4	US-09-636-215-523
9	1352	98.8	254	4	US-09-685-166A-523
10	1352	98.8	254	4	US-09-679-426-523
11	1352	98.8	254	4	US-09-759-143-523
12	1352	98.8	254	4	US-09-651-236-523
13	1205	88.0	449	4	US-09-636-215-617
14	1205	88.0	449	4	US-09-685-166A-617
15	1205	88.0	449	4	US-09-679-426-617
16	1205	88.0	449	4	US-09-759-143-617
17	1205	88.0	449	4	US-09-651-236-617
18	1185	86.6	220	3	US-09-439-313-327
19	1185	86.6	220	3	US-09-352-616A-327
20	1185	86.6	220	4	US-09-232-149A-327
21	1185	86.6	220	4	US-09-636-215-327
22	1185	86.6	220	4	US-09-685-166A-327
23	1185	86.6	220	4	US-09-688-489-327
24	1185	86.6	220	4	US-09-679-426-327
25	1185	86.6	220	4	US-09-759-143-327
26	1185	86.6	220	4	US-09-651-236-327
27	1167.5	85.3	284	4	US-09-386-642-54

28	1160	84.7	248	1	US-08-744-026-1	Sequence 1, Appli
29	1160	84.7	248	2	US-09-102-732-1	Sequence 1, Appli
30	1160	84.7	248	3	US-09-261-767-1	Sequence 1, Appli
31	1124	82.1	232	2	US-08-897-340-31	Sequence 31, Appl
32	1124	82.1	232	3	US-09-252-329-31	Sequence 31, Appl
33	1070	78.2	205	3	US-09-020-956-176	Sequence 176, App
34	1070	78.2	205	3	US-09-030-607-176	Sequence 176, App
35	1070	78.2	205	3	US-09-439-313-176	Sequence 176, App
36	1070	78.2	205	3	US-09-352-616A-176	Sequence 176, App
37	1070	78.2	205	4	US-09-232-149A-176	Sequence 176, App
38	1070	78.2	205	4	US-09-159-812-176	Sequence 176, App
39	1070	78.2	205	4	US-09-636-215-176	Sequence 176, App
40	1070	78.2	205	4	US-09-685-166A-176	Sequence 176, App
41	1070	78.2	205	4	US-09-115-453-176	Sequence 176, App
42	1070	78.2	205	4	US-09-688-489-176	Sequence 176, App
43	1070	78.2	205	4	US-09-679-426-176	Sequence 176, App
44	1070	78.2	205	4	US-09-759-143-176	Sequence 176, App
45	1070	78.2	205	4	US-09-651-236-176	Sequence 176, App

ALIGNMENTS

RESULT 1
US-09-439-313-525
; Sequence 525, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 525
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-439-313-525

Query Match	100.0%;	Score 1369;	DB 3;	Length 254;
Best Local Similarity	100.0%;	Pred. No. 2.8e-132;	Indels	0;
Matches	254;	Conservative	0;	Mismatches
QY	1	MATAGNPGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPWQAALVMENELFCSGYL	60	
Db	1	MATAGNPGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPWQAALVMENELFCSGYL	60	
QY	61	VHPQWLSAAHCFQNSYITIGLHLSLEADQEPGSMVEASLSVRHPEYNRPLLANDLMLI	120	
Db	61	VHPQWLSAAHCFQNSYITIGLHLSLEADQEPGSMVEASLSVRHPEYNRPLLANDLMLI	120	
QY	121	KLDESVSSEDTRISIASOCTAGNSCLVSGWGLANGMPVLQCVNVSVVSEVCSK	180	
Db	121	KLDESVSSEDTRISIASOCTAGNSCLVSGWGLANGMPVLQCVNVSVVSEVCSK	180	
QY	181	LYDPLYPHSMFCAGGGQDKSCNGDGGPLICNGYLOGLVSFGKAPCGQGVPGVYTNL	240	
Db	181	LYDPLYPHSMFCAGGGQDKSCNGDGGPLICNGYLOGLVSFGKAPCGQGVPGVYTNL	240	
QY	241	CKFTEWIKTVQAS	254	

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Db 241 CKFTWIEKTVQAS 254
|||||
RESULT 2
US-09-636-215-525
; Sequence 525, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 525
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-636-215-525

Query Match 100.0%; Score 1369; DB 4; Length 254;
Best Local Similarity 100.0%; Pred. No. 2.8e-132;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATAGNPMGWFLGYLILGVAGSLVSGSCSIINGEDCSPHSQPWOAALVMENELFCSGVL 60
|
Db 1 MATAGNPMGWFLGYLILGVAGSLVSGSCSIINGEDCSPHSQPWOAALVMENELFCSGVL 60
|
QY 61 VHPQWVLSAAHCFQNSYTTIGLGLHSLVAGSLVSGSCSIINGEDCSPHSQPWOAALVMENELFCSGVL 120
|
Db 61 VHPQWVLSAAHCFQNSYTTIGLGLHSLVAGSLVSGSCSIINGEDCSPHSQPWOAALVMENELFCSGVL 120
|
QY 121 KLDSESVESDTRISISIAQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
|
Db 121 KLDSESVESDTRISISIAQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
|
QY 181 LYDPLVHPSMFCAGGQDQKDCNCGDSGGPLICNGYLOGLVSGFKAPCGQVGPVGYTNL 240
|
Db 181 LYDPLVHPSMFCAGGQDQKDCNCGDSGGPLICNGYLOGLVSGFKAPCGQVGPVGYTNL 240
|
QY 241 CKFTWIEKTVQAS 254
|
Db 241 CKFTWIEKTVQAS 254
|

RESULT 3
US-09-685-166A-525
; Sequence 525, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.

Query Match 100.0%; Score 1369; DB 4; Length 254;
Best Local Similarity 100.0%; Pred. No. 2.8e-132;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATAGNPMGWFLGYLILGVAGSLVSGSCSIINGEDCSPHSQPWOAALVMENELFCSGVL 60
|
Db 1 MATAGNPMGWFLGYLILGVAGSLVSGSCSIINGEDCSPHSQPWOAALVMENELFCSGVL 60
|
QY 61 VHPQWVLSAAHCFQNSYTTIGLGLHSLVAGSLVSGSCSIINGEDCSPHSQPWOAALVMENELFCSGVL 120
|
Db 61 VHPQWVLSAAHCFQNSYTTIGLGLHSLVAGSLVSGSCSIINGEDCSPHSQPWOAALVMENELFCSGVL 120
|
QY 121 KLDSESVESDTRISISIAQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
|
Db 121 KLDSESVESDTRISISIAQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
|
QY 181 LYDPLVHPSMFCAGGQDQKDCNCGDSGGPLICNGYLOGLVSGFKAPCGQVGPVGYTNL 240
|
Db 181 LYDPLVHPSMFCAGGQDQKDCNCGDSGGPLICNGYLOGLVSGFKAPCGQVGPVGYTNL 240
|
QY 241 CKFTWIEKTVQAS 254
|
Db 241 CKFTWIEKTVQAS 254
|

RESULT 4
US-09-679-426-525
; Sequence 525, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
```

;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;; FILE REFERENCE: 210121.427C20
;; CURRENT APPLICATION NUMBER: US/09/679,426
;; CURRENT FILING DATE: 2000-10-02
;; NUMBER OF SEQ ID NOS: 895
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 525
;; LENGTH: 254
;; TYPE: PRT
;; ORGANISM: Homo sapien
US-09-679-426-525

Query Match 100.0%; Score 1369; DB 4; Length 254;
Best Local Similarity 100.0%; Pred. No. 2.8e-132;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATAGNPGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPQWQAALVWENELFCSGYL 60
DB 1 MATAGNPGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPQWQAALVWENELFCSGYL 60
QY 61 VHPQWVLSAAHCFQNSYTTIGLGLHSLSEADQEPGQSMVEASLSVRHPEYNRPLLANDMLI 120
DB 61 VHPQWVLSAAHCFQNSYTTIGLGLHSLSEADQEPGQSMVEASLSVRHPEYNRPLLANDMLI 120
QY 121 KLDESVSSEDTIRSIASQCPAGNSCLVSGWGLLANGRMPTVLQCVNVSVSEVCSK 180
DB 121 KLDESVSSEDTIRSIASQCPAGNSCLVSGWGLLANGRMPTVLQCVNVSVSEVCSK 180
QY 181 LYDPLVHPSMFCAGGQDQKDCNCGDSGGPLICNGYLOGLVSGFKAPCGQVGPVYTNL 240
DB 181 LYDPLVHPSMFCAGGQDQKDCNCGDSGGPLICNGYLOGLVSGFKAPCGQVGPVYTNL 240
QY 241 CKFTEWIEKTVQAS 254
DB 241 CKFTEWIEKTVQAS 254

RESULT 5
US-09-759-143-525
; Sequence 525, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 525
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-759-143-525

Query Match 100.0%; Score 1369; DB 4; Length 254;
Best Local Similarity 100.0%; Pred. No. 2.8e-132;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATAGNPGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPQWQAALVWENELFCSGYL 60
DB 1 MATAGNPGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPQWQAALVWENELFCSGYL 60
QY 61 VHPQWVLSAAHCFQNSYTTIGLGLHSLSEADQEPGQSMVEASLSVRHPEYNRPLLANDMLI 120
DB 61 VHPQWVLSAAHCFQNSYTTIGLGLHSLSEADQEPGQSMVEASLSVRHPEYNRPLLANDMLI 120
QY 121 KLDESVSSEDTIRSIASQCPAGNSCLVSGWGLLANGRMPTVLQCVNVSVSEVCSK 180
DB 121 KLDESVSSEDTIRSIASQCPAGNSCLVSGWGLLANGRMPTVLQCVNVSVSEVCSK 180
QY 181 LYDPLVHPSMFCAGGQDQKDCNCGDSGGPLICNGYLOGLVSGFKAPCGQVGPVYTNL 240
DB 181 LYDPLVHPSMFCAGGQDQKDCNCGDSGGPLICNGYLOGLVSGFKAPCGQVGPVYTNL 240
QY 241 CKFTEWIEKTVQAS 254
DB 241 CKFTEWIEKTVQAS 254
RESULT 6
US-09-651-236-525
; Sequence 525, Application US/09651236
; Patent No. 6818751
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42718C18
; CURRENT APPLICATION NUMBER: US/09/651,236
; CURRENT FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 865
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 525
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-651-236-525

Query Match 100.0%; Score 1369; DB 4; Length 254;
Best Local Similarity 100.0%; Pred. No. 2.8e-132;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATAGNPGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPQWQAALVWENELFCSGYL 60
DB 1 MATAGNPGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPQWQAALVWENELFCSGYL 60
QY 61 VHPQWVLSAAHCFQNSYTTIGLGLHSLSEADQEPGQSMVEASLSVRHPEYNRPLLANDMLI 120
DB 61 VHPQWVLSAAHCFQNSYTTIGLGLHSLSEADQEPGQSMVEASLSVRHPEYNRPLLANDMLI 120
QY 121 KLDESVSSEDTIRSIASQCPAGNSCLVSGWGLLANGRMPTVLQCVNVSVSEVCSK 180

Db 121 KLDSESVESDTRISISQCTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
QY 181 LYDPLVHPSMFCAGGQDQKSCNGSDGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
Db 181 LYDPLVHPSMFCAGGQDQKSCNGSDGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
QY 241 CKFTWIEKTVQAS 254
Db 241 CKFTWIEKTVQAS 254

RESULT 7

US-09-439-313-523

; Sequence 523, Application US/09439313

; Patent No. 6329505

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan Louise

; APPLICANT: Jiang Yuqui

; APPLICANT: Reed, Steven G.

; APPLICANT: Kalos, Michael

; APPLICANT: Fanger, Gary

; APPLICANT: Retter, Mark

; APPLICANT: Solk, John

; APPLICANT: Day, Craig

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.427C9

; CURRENT APPLICATION NUMBER: US/09/439,313

; CURRENT FILING DATE: 1999-11-12

; NUMBER OF SEQ ID NOS: 575

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 523

; LENGTH: 254

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Made in a lab

; NAME/KEY: VARIANT

; LOCATION: (1)...(254)

; OTHER INFORMATION: Xaa = Any amino acid

US-09-439-313-523

Query Match 98.8%; Score 1352; DB 3; Length 254;
Best Local Similarity 98.8%; Pred. No. 1.6e-130;
Matches 251; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MATAGNPWGFWFLGYLLGVAGSLVSGSCSQIINGEDCSPHSQPWOAALVMENELFCSGYL 60
Db 1 MATAGNPWGFWFLGYLLGVAGSLVSGSCSQIINGEDCSPHSQPWOAALVMENELFCSGYL 60
QY 61 VHPQWLSAAHCFQNSYTTIGLHLSLEADQEPGSMVEASLSVRHPEYNRPRLANDLMLI 120
Db 61 VHPQWLSATHCFQNSYTTIGLHLSLEADQEPGSMVEASLSVRHPEYNRPRLANDLMLI 120
QY 121 KLDSESVESDTRISISQCTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
Db 121 KLDSESVESDTRISISQCTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
QY 181 LYDPLVHPSMFCAGGQDQKSCNGSDGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
Db 181 LYDPLVHPSMFCAGGQDQKSCNGSDGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
QY 241 CKFTWIEKTVQAS 254
Db 241 CKFTWIEKTVQAS 254

RESULT 8

US-09-636-215-523

; Sequence 523, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 523
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
; NAME/KEY: VARIANT
; LOCATION: (1)...(254)
; OTHER INFORMATION: Xaa = any amino acid
US-09-636-215-523

Query Match 98.8%; Score 1352; DB 4; Length 254;
Best Local Similarity 98.8%; Pred. No. 1.6e-130;
Matches 251; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MATAGNPWGFWFLGYLLGVAGSLVSGSCSQIINGEDCSPHSQPWOAALVMENELFCSGYL 60
Db 1 MATAGNPWGFWFLGYLLGVAGSLVSGSCSQIINGEDCSPHSQPWOAALVMENELFCSGYL 60
QY 61 VHPQWLSAAHCFQNSYTTIGLHLSLEADQEPGSMVEASLSVRHPEYNRPRLANDLMLI 120
Db 61 VHPQWLSATHCFQNSYTTIGLHLSLEADQEPGSMVEASLSVRHPEYNRPRLANDLMLI 120
QY 121 KLDSESVESDTRISISQCTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
Db 121 KLDSESVESDTRISISQCTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
QY 181 LYDPLVHPSMFCAGGQDQKSCNGSDGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
Db 181 LYDPLVHPSMFCAGGQDQKSCNGSDGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
QY 241 CKFTWIEKTVQAS 254
Db 241 CKFTWIEKTVQAS 254

RESULT 9

US-09-685-166A-523

; Sequence 523, Application US/09685166A

; Patent No. 6630305

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqui

```
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 523
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
; NAME/KEY: VARIANT
; LOCATION: (1)...(254)
; OTHER INFORMATION: Xaa = any amino acid
US-09-685-166A-523

Query Match          98.8%; Score 1352; DB 4; Length 254;
Best Local Similarity 98.8%; Pred. No. 1.6e-130;
Matches 251; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MATAGNPMGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPWQAALVMENELFCSGYL 60
DB 1 MATAGNPMGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPWQAALVMENELFCSGYL 60

QY 61 VHPQWLSAAHCFQNSYTTIGLHLSLEADQEPGSMVEASLSVRHPEYNRPLLANDMLI 120
DB 61 VHPQWLSATHCFQNSYTTIGLHLSLEADQEPGSMVEASLSVRHPEYNRPLLANDMLI 120

QY 121 KLDESVSSEDTIRSIASQCPAGNSCLVSGGGLANGRMPVTLQCVNVSVVSEVCSK 180
DB 121 KLDESVSSEDTIRSIASQCPAGNSCLVSGGGLANGRMPVTLQCVNVSVVSEVCSK 180

QY 181 LYDPLYPHSMFCAGGGQXODKSCNGSDGGPLICNGYLOGLVSGKAPCGQGVPGVYTNL 240
DB 181 LYDPLYPHSMFCAGGGQXODKSCNGSDGGPLICNGYLOGLVSGKAPCGQGVPGVYTNL 240

QY 241 CKFTWIEKTVQAS 254
DB 241 CKFTWIEKTVQAS 254

RESULT 10
US-09-679-426-523
; Sequence 523, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
```

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; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C20
; CURRENT APPLICATION NUMBER: US/09/679,426
; CURRENT FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 895
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 523
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
; NAME/KEY: VARIANT
; LOCATION: (1)...(254)
; OTHER INFORMATION: Xaa = any amino acid
US-09-679-426-523

Query Match          98.8%; Score 1352; DB 4; Length 254;
Best Local Similarity 98.8%; Pred. No. 1.6e-130;
Matches 251; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MATAGNPMGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPWQAALVMENELFCSGYL 60
DB 1 MATAGNPMGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPWQAALVMENELFCSGYL 60

QY 61 VHPQWLSAAHCFQNSYTTIGLHLSLEADQEPGSMVEASLSVRHPEYNRPLLANDMLI 120
DB 61 VHPQWLSATHCFQNSYTTIGLHLSLEADQEPGSMVEASLSVRHPEYNRPLLANDMLI 120

QY 121 KLDESVSSEDTIRSIASQCPAGNSCLVSGGGLANGRMPVTLQCVNVSVVSEVCSK 180
DB 121 KLDESVSSEDTIRSIASQCPAGNSCLVSGGGLANGRMPVTLQCVNVSVVSEVCSK 180

QY 181 LYDPLYPHSMFCAGGGQXODKSCNGSDGGPLICNGYLOGLVSGKAPCGQGVPGVYTNL 240
DB 181 LYDPLYPHSMFCAGGGQXODKSCNGSDGGPLICNGYLOGLVSGKAPCGQGVPGVYTNL 240

QY 241 CKFTWIEKTVQAS 254
DB 241 CKFTWIEKTVQAS 254

RESULT 11
US-09-759-143-523
; Sequence 523, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
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; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 523
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
; NAME/KEY: VARIANT
; LOCATION: (1)...(254)
; OTHER INFORMATION: Xaa = any amino acid
US-09-759-143-523

Query Match 98.8%; Score 1352; DB 4; Length 254;
Best Local Similarity 98.8%; Pred. No. 1.6e-130;
Matches 251; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MATAGNPMGWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWQAALVMENELFCSGYL 60
DB 1 MATAGNPMGWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWQAALVMENELFCSGYL 60
QY 61 VHPQWLVAACHCFQNSYITIGLHLSLEADQEPGSMVEASLSVRHPEYRNPRLANDMLI 120
DB 61 VHPQWLVAACHCFQNSYITIGLHLSLEADQEPGSMVEASLSVRHPEYRNPRLANDMLI 120
QY 121 KLDSESVESDTRISISQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVSEVCSK 180
DB 121 KLDSESVESDTRISISQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVSEVCSK 180
QY 181 LYDPLYPHSMFCAGGQXQXDSGNGSGGPLICNGYLQGLVSGFKAPCGQVGPVGYTNL 240
DB 181 LYDPLYPHSMFCAGGQXQXDSGNGSGGPLICNGYLQGLVSGFKAPCGQVGPVGYTNL 240
QY 241 CKFTWIEKTVQAS 254
DB 241 CKFTWIEKTVQAS 254

RESULT 12
US-09-651-236-523

; Sequence 523, Application US/09651236
; Patent No. 6818751

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.42718C18

; CURRENT APPLICATION NUMBER: US/09/651,236

; CURRENT FILING DATE: 2000-08-29

; NUMBER OF SEQ ID NOS: 865

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 523

; LENGTH: 254

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Made in a lab
; NAME/KEY: VARIANT
; LOCATION: (1)...(254)
; OTHER INFORMATION: Xaa = any amino acid
US-09-651-236-523

Query Match 98.8%; Score 1352; DB 4; Length 254;
Best Local Similarity 98.8%; Pred. No. 1.6e-130;
Matches 251; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MATAGNPMGWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWQAALVMENELFCSGYL 60
DB 1 MATAGNPMGWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWQAALVMENELFCSGYL 60
QY 61 VHPQWLVAACHCFQNSYITIGLHLSLEADQEPGSMVEASLSVRHPEYRNPRLANDMLI 120
DB 61 VHPQWLVAACHCFQNSYITIGLHLSLEADQEPGSMVEASLSVRHPEYRNPRLANDMLI 120
QY 121 KLDSESVESDTRISISQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVSEVCSK 180
DB 121 KLDSESVESDTRISISQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVSEVCSK 180
QY 181 LYDPLYPHSMFCAGGQXQXDSGNGSGGPLICNGYLQGLVSGFKAPCGQVGPVGYTNL 240
DB 181 LYDPLYPHSMFCAGGQXQXDSGNGSGGPLICNGYLQGLVSGFKAPCGQVGPVGYTNL 240
QY 241 CKFTWIEKTVQAS 254
DB 241 CKFTWIEKTVQAS 254

RESULT 13

US-09-636-215-617

; Sequence 617, Application US/09636215

; Patent No. 6620922

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.42717C17

; CURRENT APPLICATION NUMBER: US/09/636,215

; CURRENT FILING DATE: 2000-08-10

; NUMBER OF SEQ ID NOS: 852

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 617

; LENGTH: 449

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-636-215-617

Query Match 88.0%; Score 1205; DB 4; Length 449;
Best Local Similarity 100.0%; Pred. No. 4.3e-115;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 31 IINGEDCSPHSQPWQAALVMENELFCSGVLVHPQWVLSAAHCFQNSYITIGLHLSLEADQ 90
DB 8 IINGEDCSPHSQPWQAALVMENELFCSGVLVHPQWVLSAAHCFQNSYITIGLHLSLEADQ 67

QY 91 EPGSQMVEASLSVRHPEYNRPPLANDMLIKLDESVSSESDTIRSIASQCPPTAGNSCLV 150
Db 68 EPGSQMVEASLSVRHPEYNRPPLANDMLIKLDESVSSESDTIRSIASQCPPTAGNSCLV 127
QY 151 SGWGLLANGRMPTVLQCVNVSVVSEVCSKLYDPLYPHPSMFCAGGGQDQKDCNCGDSGGP 210
Db 128 SGWGLLANGRMPTVLQCVNVSVVSEVCSKLYDPLYPHPSMFCAGGGQDQKDCNCGDSGGP 187
QY 211 LICNGYLOGLVSFGKAPCGQGVPGVYTNLCKFTWIEKTVQAS 254
Db 188 LICNGYLOGLVSFGKAPCGQGVPGVYTNLCKFTWIEKTVQAS 231

RESULT 14

US-09-685-166A-617
; Sequence 617, Application US/09685166A

; Patent No. 6630305

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqui

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.427C21

; CURRENT APPLICATION NUMBER: US/09/685,166A

; CURRENT FILING DATE: 2000-10-10

; NUMBER OF SEQ ID NOS: 898

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 617

; LENGTH: 449

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-685-166A-617

Query Match 88.0%; Score 1205; DB 4; Length 449;
Best Local Similarity 100.0%; Pred. No. 4.3e-115;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 IINGEDCSPHSQPWOAALVMENELFCSGVLVHPQWVLSAAHCFQNSYTTIGLHLSLEADQ 90
Db 8 IINGEDCSPHSQPWOAALVMENELFCSGVLVHPQWVLSAAHCFQNSYTTIGLHLSLEADQ 67
QY 91 EPGSQMVEASLSVRHPEYNRPPLANDMLIKLDESVSSESDTIRSIASQCPPTAGNSCLV 150
Db 68 EPGSQMVEASLSVRHPEYNRPPLANDMLIKLDESVSSESDTIRSIASQCPPTAGNSCLV 127
QY 151 SGWGLLANGRMPTVLQCVNVSVVSEVCSKLYDPLYPHPSMFCAGGGQDQKDCNCGDSGGP 210
Db 128 SGWGLLANGRMPTVLQCVNVSVVSEVCSKLYDPLYPHPSMFCAGGGQDQKDCNCGDSGGP 187
QY 211 LICNGYLOGLVSFGKAPCGQGVPGVYTNLCKFTWIEKTVQAS 254
Db 188 LICNGYLOGLVSFGKAPCGQGVPGVYTNLCKFTWIEKTVQAS 231

RESULT 15

US-09-679-426-617

; Sequence 617, Application US/09679426

; Patent No. 6759515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C20
; CURRENT APPLICATION NUMBER: US/09/679,426
; CURRENT FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 895
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 617
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-679-426-617

Query Match 88.0%; Score 1205; DB 4; Length 449;
Best Local Similarity 100.0%; Pred. No. 4.3e-115;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 IINGEDCSPHSQPWOAALVMENELFCSGVLVHPQWVLSAAHCFQNSYTTIGLHLSLEADQ 90
Db 8 IINGEDCSPHSQPWOAALVMENELFCSGVLVHPQWVLSAAHCFQNSYTTIGLHLSLEADQ 67
QY 91 EPGSQMVEASLSVRHPEYNRPPLANDMLIKLDESVSSESDTIRSIASQCPPTAGNSCLV 150
Db 68 EPGSQMVEASLSVRHPEYNRPPLANDMLIKLDESVSSESDTIRSIASQCPPTAGNSCLV 127
QY 151 SGWGLLANGRMPTVLQCVNVSVVSEVCSKLYDPLYPHPSMFCAGGGQDQKDCNCGDSGGP 210
Db 128 SGWGLLANGRMPTVLQCVNVSVVSEVCSKLYDPLYPHPSMFCAGGGQDQKDCNCGDSGGP 187
QY 211 LICNGYLOGLVSFGKAPCGQGVPGVYTNLCKFTWIEKTVQAS 254
Db 188 LICNGYLOGLVSFGKAPCGQGVPGVYTNLCKFTWIEKTVQAS 231

Search completed: February 10, 2005, 08:55:49
Job time : 42 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2005, 08:36:55 ; Search time 166 Seconds
(without alignments)
591.790 Million cell updates/sec

Title: US-09-895-814-525
Perfect score: 1369
Sequence: 1 MATAGNPGWFLGYLILGVA.....GVYTNLCKFTWIKTVOAS 254

Scoring table: BLASTUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1369	100.0	254	3 AAB21294	Aab21294 Human KLK
2	1369	100.0	254	4 AAM01174	Aam01174 Human pro
3	1369	100.0	254	4 AAU69819	Aau69819 Human pro
4	1369	100.0	254	4 AAG99059	Aag99059 Human pro
5	1369	100.0	254	4 ABU71710	Abu71710 Prostate
6	1369	100.0	254	5 ABB95279	Abb95279 Human P70
7	1369	100.0	254	6 ABP54360	Abp54360 Human KLK
8	1369	100.0	254	6 ABP54357	Abp54357 Human KLK
9	1369	100.0	254	6 ABR54391	Abt54391 Prostate
10	1369	100.0	254	7 ADB13975	Adb13975 Human pro
11	1369	100.0	254	7 ADG26391	Adg26391 Human pro
12	1369	100.0	1079	4 AAB74830	Aab74830 Prostate
13	1369	100.0	1079	4 ABU71860	Abu71860 Prostate
14	1364	99.6	254	3 AAB21320	Aab21320 Human pro
15	1364	99.6	254	4 AAU72525	Aau72525 Human pro
16	1364	99.6	254	5 AAU74901	Aau74901 Protein s
17	1364	99.6	254	5 AAU74932	Aau74932 Amino aci
18	1352	98.8	254	4 AAM01173	Aam01173 Human pro
19	1352	98.8	254	4 AAU69818	Aau69818 Human pro
20	1352	98.8	254	4 AAG99058	Aag99058 Human pro
21	1352	98.8	254	4 AAB95278	Abb95278 Human P70
22	1352	98.8	254	5 ABB95278	Abb95278 Human P70
23	1352	98.8	254	6 ABR54390	Abt54390 Prostate
24	1352	98.8	254	7 ADB13973	Adb13973 Human mat
25	1352	98.8	254	7 ADG26389	Adg26389 Human pro

26	1352	98.8	258	3 AAB21324	Aab21324 Human EMS
27	1342	98.0	249	3 AAB21307	Aab21307 Human pro
28	1330	97.2	253	3 AAB21308	Aab21308 Human EMS
29	1255	91.7	234	4 AAE00397	Aae00397 Human ser
30	1241	90.7	231	2 AAY25510	Aay25510 Human pro
31	1237	90.4	237	3 AAB21293	Aab21293 Human KLK
32	1205	88.0	449	4 AAM01227	Aam01227 P703P and
33	1205	88.0	449	4 AAU69872	Aau69872 Human pro
34	1205	88.0	449	4 ABU71763	Abu71763 Prostate
35	1205	88.0	449	5 ABB95332	Abb95332 Human P70
36	1205	88.0	449	6 ABR54444	Abt54444 Prostate
37	1205	88.0	449	7 ADB14067	Adb14067 Human pro
38	1205	88.0	449	7 ADG26483	Adg26483 Human pro
39	1205	88.0	585	4 ABU71889	Abu71889 Prostate
40	1205	88.0	585	4 ABR54580	Abt54580 Prostate
41	1205	88.0	585	7 ADB14470	Adb14470 FOPP/hpAP
42	1205	88.0	585	7 ADG26593	Adg26593 Human pro
43	1205	88.0	801	4 ABU71890	Abu71890 Prostate
44	1205	88.0	801	4 AAY72526	Aay72526 Human pro
45	1191	87.0	226	4 AAY72526	Aay72526 Human pro

ALIGNMENTS

RESULT 1
AAB21294
ID AAB21294 standard; protein; 254 AA.
XX
AC AAB21294;
XX
DT 02-FEB-2001 (first entry)
XX
DE Human KLK-L1 protein #2.
XX
KW Human; KLK-L1; KLK-L2; KLK-L3; KLK-L4; KLK-L5; KLK-L6;
KW kallikrein-like protein; serine protease; cytosolic; cancer;
KW prostate cancer.
XX
OS Homo sapiens.
XX
PN WO2000053776-A2.
XX
PD 14-SEP-2000.
XX
PF 09-MAR-2000; 2000WO-CA000258.
XX
PR 11-MAR-1999; 99US-0124260P.
PR 01-APR-1999; 99US-0127386P.
PR 21-JUL-1999; 99US-0144919P.
PA (MOUN) MOUNT SINAI HOSPITAL.
PI Yousef GM, Diamandis EP;
XX
XX WPI; 2000-587440/55.
XX N-PSDB; AAA95896.
PT New kallikrein-like (KLK-L) proteins for diagnosing and treating KLK-L
XX protein mediated disorders, especially cancer.
XX
XX Claim 8; Page 141; 184pp; English.
XX
XX The present sequence is kallikrein-like protein KLK-L1. Kallikreins and
XX kallikrein-like proteins are a subgroup of the serine protease enzyme
XX family. They catalyse the selective cleavage of specific polypeptide
XX precursors to release peptides with potent biological activity. Nucleic
XX acids encoding kallikrein-like proteins KLK-L1, KLK-L2, KLK-L3, KLK-L4,
XX KLK-L5 and KLK-L6 have been isolated. The proteins are useful in the
XX treatment, monitoring and diagnosis of cancers, especially prostate
XX cancer. They can also be used to identify a substance that can associate
XX with or mediate the biological activity of the proteins. Antibodies can
XX be used to treat conditions mediated by the kallikrein-like proteins

XX SQ Sequence 254 AA;
Query Match 100.0%; Score 1369; DB 3; Length 254;
Best Local Similarity 100.0%; Pred. No. 8.6e-96;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATAGNPWGFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPQWQAALVMENELFCSGVL 60
DB 1 MATAGNPWGFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPQWQAALVMENELFCSGVL 60
QY 61 VHPQWVLSAAHCFQNSYITIGLHLSLEADQEPGQSMVEASLSVRHPEYRNPRLANDLMLI 120
DB 61 VHPQWVLSAAHCFQNSYITIGLHLSLEADQEPGQSMVEASLSVRHPEYRNPRLANDLMLI 120
QY 121 KLDSESVESDTIRSIASQCPAGNSCLVSGWGLLANGMPVTLCVNVSVSEVCSK 180
DB 121 KLDSESVESDTIRSIASQCPAGNSCLVSGWGLLANGMPVTLCVNVSVSEVCSK 180
QY 181 LYDPLYPHSMFCAGGQDQKDSNGSGGLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
DB 181 LYDPLYPHSMFCAGGQDQKDSNGSGGLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
QY 241 CKFTWIEKTVQAS 254
DB 241 CKFTWIEKTVQAS 254

RESULT 2
AAU01174
ID AAU01174 standard; protein; 254 AA.
XX AAU01174;
XX
DT 04-OCT-2001 (first entry)
DE Human prostate-specific amino acid sequence P703P.
XX
KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KW cytostatic; gene therapy; metastasis.
XX
OS Homo sapiens.
XX
PN WO200151633-A2.
PD 19-JUL-2001.
PF 16-JAN-2001; 2001WO-US001574.
XX
PR 14-JAN-2000; 2000US-00483672.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
PI Wang A, Meagher MJ;
XX
DR WPI; 2001-425873/45.
XX
PT New polynucleotide encoding a prostate-specific protein, for diagnosing,
PT monitoring and treating prostate cancer in a patient and for use in
PT vaccines.
XX
PS Claim 2; Page 405; 543pp; English.
XX

CC The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated T cells
CC prepared using (I) or (II) are used to treat cancer in a patient. (I) and
CC the antibodies are also used in the detection of cancer in a patient. The
CC cancer that is diagnosed or treated is particularly prostate cancer. (I)
CC and (II) can be used in vaccines. The antibodies or (I) can be used for

CC monitoring the progression of cancer in a patient. (I) and (II) can also
CC be used to improve diagnostic and therapeutic methods for prostate
CC cancer. They can indicate the level of metastasis as well as the prostate
CC volume. AAH93357 to AAH93944 and AAU01115 to AAU01318 represent
CC polynucleotide and amino acid sequences used in the exemplification of
CC the present invention
XX

SQ Sequence 254 AA;
Query Match 100.0%; Score 1369; DB 4; Length 254;
Best Local Similarity 100.0%; Pred. No. 8.6e-96;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATAGNPWGFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPQWQAALVMENELFCSGVL 60
DB 1 MATAGNPWGFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPQWQAALVMENELFCSGVL 60
QY 61 VHPQWVLSAAHCFQNSYITIGLHLSLEADQEPGQSMVEASLSVRHPEYRNPRLANDLMLI 120
DB 61 VHPQWVLSAAHCFQNSYITIGLHLSLEADQEPGQSMVEASLSVRHPEYRNPRLANDLMLI 120
QY 121 KLDSESVESDTIRSIASQCPAGNSCLVSGWGLLANGMPVTLCVNVSVSEVCSK 180
DB 121 KLDSESVESDTIRSIASQCPAGNSCLVSGWGLLANGMPVTLCVNVSVSEVCSK 180
QY 181 LYDPLYPHSMFCAGGQDQKDSNGSGGLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
DB 181 LYDPLYPHSMFCAGGQDQKDSNGSGGLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
QY 241 CKFTWIEKTVQAS 254
DB 241 CKFTWIEKTVQAS 254

RESULT 3
AAU69819
ID AAU69819 standard; protein; 254 AA.
XX AAU69819;
XX
DT 30-JAN-2002 (first entry)
DE Human prostate cDNA encoded protein #27.
XX
KW Human; prostate cancer; cytostatic; immunostimulant; tumour; immunogen.
XX
OS Homo sapiens.
XX
PN WO200173032-A2.
XX
PD 04-OCT-2001.
XX
PF 27-MAR-2001; 2001WO-US009919.
XX
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 09-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
PR 09-NOV-2000; 2000US-00709729.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedwick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
DR WPI; 2001-639232/73.

DR N-PSDB; AAS63914.
 XX New human prostate-specific polypeptides and polynucleotides useful for
 PT the diagnosis and treatment of cancer, especially prostate cancer.
 XX
 XX Claim 2; Page 405-406; 579pp; English.
 XX
 XX The invention relates to isolated prostate-specific polynucleotides,
 CC polypeptides, fusion proteins of the polypeptides, antibodies raised
 CC against the polypeptides (or antigenic epitopes derived from them) and
 CC antigen-presenting cells expressing the polypeptides. The antibodies are
 CC useful for detecting the presence of cancer, especially prostate cancer.
 CC The polypeptides, polynucleotides and the antigen-presenting cells are
 CC useful for stimulating and/or expanding T cells specific for a tumour
 CC protein, and for inhibiting the development of cancer especially prostate
 CC cancer. Compositions comprising the polynucleotide and/or polypeptide are
 CC useful for stimulating an immune response, and for treating cancer. The
 CC oligonucleotide is useful for detecting cancer. The present sequence is a
 CC prostate specific polypeptide of the invention
 XX
 SQ Sequence 254 AA;
 Query Match 100.0%; Score 1369; DB 4; Length 254;
 Best Local Similarity 100.0%; Pred. No. 8.6e-96;
 Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MATAGNPGWFLGYLLGVAGSLVSGSCSQIINGEDCSPHSQPQWQAALVMENELFCSGVL 60
 Db 1 MATAGNPGWFLGYLLGVAGSLVSGSCSQIINGEDCSPHSQPQWQAALVMENELFCSGVL 60
 QY 61 VHPQWLSAAHCFQNSYTTGLGLHSLEADQEPGQWVEASLSVRHPEYRPLLANDMLI 120
 Db 61 VHPQWLSAAHCFQNSYTTGLGLHSLEADQEPGQWVEASLSVRHPEYRPLLANDMLI 120
 QY 121 KLDSEVSSEDTRISISIAQCPTAGNSCLVSGWGLLANGRMPTVLCQVNVSVSEVCSK 180
 Db 121 KLDSEVSSEDTRISISIAQCPTAGNSCLVSGWGLLANGRMPTVLCQVNVSVSEVCSK 180
 QY 181 LYDPLYPHSMFCAGGQDQKDCSCNGSGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
 Db 181 LYDPLYPHSMFCAGGQDQKDCSCNGSGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
 QY 241 CKFTEWIEKTVQAS 254
 Db 241 CKFTEWIEKTVQAS 254
 RESULT 4
 AAG99059
 ID AAG99059 standard; protein; 254 AA.
 XX
 XX AAG99059;
 XX
 XX 25-SEP-2001 (first entry)
 DT Human prostate-specific amino acid of p703P.
 DE
 XX Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
 KW Chromosome 22q11.2; prostate-specific protein; chromosome 1;
 KW prostate specific antigen; PSA.
 XX
 XX Homo sapiens.
 XX WO200134802-A2.
 XX 17-MAY-2001.
 XX
 XX 09-NOV-2000; 2000WO-US030904.
 XX
 XX 12-NOV-1999; 99US-00439313.
 PR 18-NOV-1999; 99US-00443686.
 XX
 XX (CORI-) CORIXA CORP.
 PA

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
 PI Kalos MD, Retter MW, Stolk JA, Day CH, Skeiky YAW, Wang A;
 XX WPI; 2001-308785/32.
 XX
 XX Isolated polypeptide comprising at least an immunogenic portion of a
 PT prostate-specific protein, useful in the diagnosis and therapy of
 PT prostate cancer.
 XX
 XX Claim 3; Page 304-305; 325pp; English.
 XX
 XX The present invention describes an isolated polypeptide (P1) comprising
 CC at least an immunogenic portion of a prostate-specific protein, or its
 CC variant. Also described are polynucleotides (N1) encoding (P1) and
 CC (N1) have cytostatic activity and can be used in vaccine production. The
 CC polypeptides, nucleic acids and antibodies from the present invention are
 CC useful in the diagnosis and therapy of prostate cancer. Prostate specific
 CC genes P704P, P712P, P774P, P775P and B305D are located in a genomic
 CC region on chromosome 22q11.2 known as the Cat Eye Syndrome region.
 CC Prostate specific antigen (PSA) P501S was located on chromosome 1.
 CC AAH84671 to AAH85143 and AAG99000 to AAG99077 represent polynucleotide
 CC and polypeptide sequences used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 254 AA;
 Query Match 100.0%; Score 1369; DB 4; Length 254;
 Best Local Similarity 100.0%; Pred. No. 8.6e-96;
 Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MATAGNPGWFLGYLLGVAGSLVSGSCSQIINGEDCSPHSQPQWQAALVMENELFCSGVL 60
 Db 1 MATAGNPGWFLGYLLGVAGSLVSGSCSQIINGEDCSPHSQPQWQAALVMENELFCSGVL 60
 QY 61 VHPQWLSAAHCFQNSYTTGLGLHSLEADQEPGQWVEASLSVRHPEYRPLLANDMLI 120
 Db 61 VHPQWLSAAHCFQNSYTTGLGLHSLEADQEPGQWVEASLSVRHPEYRPLLANDMLI 120
 QY 121 KLDSEVSSEDTRISISIAQCPTAGNSCLVSGWGLLANGRMPTVLCQVNVSVSEVCSK 180
 Db 121 KLDSEVSSEDTRISISIAQCPTAGNSCLVSGWGLLANGRMPTVLCQVNVSVSEVCSK 180
 QY 181 LYDPLYPHSMFCAGGQDQKDCSCNGSGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
 Db 181 LYDPLYPHSMFCAGGQDQKDCSCNGSGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
 QY 241 CKFTEWIEKTVQAS 254
 Db 241 CKFTEWIEKTVQAS 254
 RESULT 5
 ABU71710
 ID ABU71710 standard; protein; 254 AA.
 XX
 XX ABU71710;
 XX
 XX 10-JUN-2003 (first entry)
 DT Prostate cancer specific antigen P703P #7.
 DE
 XX Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
 KW immunogen; cancer; prostate specific antigen.
 KW
 XX Homo sapiens.
 OS Synthetic.
 XX US2002192763-A1.
 XX
 XX 19-DEC-2002.
 PD
 XX 29-JUN-2001; 2001US-00895793.
 PF

```
XX 04-OCT-1999; 99US-0157455P.
PR 04-OCT-2000; 2000US-00679272.
PR 28-MAR-2001; 2001US-00822827.
XX
PA (XUJJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PA (HURA/) HURAL J.
PA (MCNE/) MCNEILL P D.
PA (HOUG/) HOUGHTON R L.
PA (DBAS/) Y DE BASSOLS C V.
PA (FOYT/) FOY T M.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J;
PI McNeill PD, Houghton RL, Y De BassolsCV, Foy TM;
XX
DR WPI: 2001-245062/25.
XX
PT Prostate specific protein and its encoding polynucleotide, useful for the
PT treatment and diagnosis of prostate cancer.
XX
PS Example 3; SEQ ID NO 525; 85pp; English.
XX
CC The invention describes a fusion protein comprising at least one amino
CC acid sequence of immunogenic portions of any of the 3 sequences not
CC defined in the specification, or sequences having at least 70 or 90 %
CC sequence identity to any one of the 35 sequences defined in the USPTO web
CC site, which is encoded by any of the 4 nucleotide sequences not defined
CC in the specification. The fusion protein, composition and methods are
CC useful for diagnosing, preventing and/or treating cancer, particularly
CC prostate cancer. The proteins are useful as markers to indicate the
CC presence or absence of cancer. This is the amino acid sequence of a
CC prostate cancer specific antigen. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from the US patent office at
CC seqdata.uspto.gov/sequence.html?DocID=US20020192763
XX
SQ Sequence 254 AA;
Query Match 100.0%; Score 1369; DB 4; Length 254;
Best Local Similarity 100.0%; Pred. No. 8.6e-96; Mismatches 0; Gaps 0;
Matches 254; Conservative 0; Indels 0;
QY 1 MATAGNPGWFLGYLLGVAGSLVSGSCQIINGEDCSPHSQWQAALVWENELFCSGVL 60
Db 1 MATAGNPGWFLGYLLGVAGSLVSGSCQIINGEDCSPHSQWQAALVWENELFCSGVL 60
QY 61 VHPQWLSAAHCFQNSYTTGLGLHLSLEADQEPGQWVEASLSVRHPEYNRPLLANDMLI 120
Db 61 VHPQWLSAAHCFQNSYTTGLGLHLSLEADQEPGQWVEASLSVRHPEYNRPLLANDMLI 120
QY 121 KLDESVSBDTTRISIASQCPAGNSCLVSGWGLLANGMPVTLQCVNVSVSEVCSK 180
Db 121 KLDESVSBDTTRISIASQCPAGNSCLVSGWGLLANGMPVTLQCVNVSVSEVCSK 180
QY 181 LYDPLYHPMFAGGGQDQKDSGNGSGGGLICNGYLQGLVSGFKAPCGQGVPGVYTNL 240
Db 181 LYDPLYHPMFAGGGQDQKDSGNGSGGGLICNGYLQGLVSGFKAPCGQGVPGVYTNL 240
XX
Db 181 LYDPLYHPMFAGGGQDQKDSGNGSGGGLICNGYLQGLVSGFKAPCGQGVPGVYTNL 240
QY 241 CKFTWIEKTVQAS 254
Db 241 CKFTWIEKTVQAS 254
XX
RESULT 6
ABB95279
ID ABB95279 standard; protein; 254 AA.
XX
AC ABB95279;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human P703P putative full length protein SEQ ID NO 525.
XX
KW Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN US2002022248-A1.
XX
PD 21-FEB-2002.
XX
PF 12-JAN-2001; 2001US-00759143.
XX
PR 25-FEB-1997; 97US-00806099.
PR 01-AUG-1997; 97US-00904804.
PR 10-FEB-1998; 98US-00020956.
PR 25-FEB-1998; 98US-00030607.
PR 14-JUL-1998; 98US-00115453.
PR 23-SEP-1998; 98US-00159812.
PR 15-JAN-1999; 99US-00232149.
PR 09-APR-1999; 99US-00288946.
PR 13-JUL-1999; 99US-00352616.
PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00443686.
PR 14-JAN-2000; 2000US-00483672.
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 10-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
XX
(XUJJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS,
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
```

XX WPI; 2002-255649/30.
 XX New prostate-specific polynucleotides for diagnosing and treating
 PT diseases, in particular prostate cancer, and as markers for the
 PT progression of cancer.
 XX
 XX Claim 2; SEQ ID NO 525; 87pp; English.
 XX The present invention provides prostate-specific coding sequences and
 CC their encoded proteins. These can be used in the diagnosis and treatment
 CC of cancers, particularly prostate cancer. The present sequence is a
 CC protein described in the invention
 XX
 SQ Sequence 254 AA;
 Query Match 100.0%; Score 1369; DB 5; Length 254;
 Best Local Similarity 100.0%; Pred. No. 8.6e-96;
 Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MATAGNPWGFWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWQAALVMENELFCGVL 60
 DB 1 MATAGNPWGFWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWQAALVMENELFCGVL 60
 QY 61 VHPQWVLSAAHCFQNSYTTIGLHLSLEADQEPGSMVEASLSVRHPEYRPLLANDMLI 120
 DB 61 VHPQWVLSAAHCFQNSYTTIGLHLSLEADQEPGSMVEASLSVRHPEYRPLLANDMLI 120
 QY 121 KLDESSESDDTIRSIASQCTAGNSCLVSGWGLLANGRMPTVLCVNVSVSEVCSK 180
 DB 121 KLDESSESDDTIRSIASQCTAGNSCLVSGWGLLANGRMPTVLCVNVSVSEVCSK 180
 QY 181 LYDPLYPHPSMFCAGGGQDQKDSNGDSGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
 DB 181 LYDPLYPHPSMFCAGGGQDQKDSNGDSGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
 QY 241 CKTEWIEKTQVAS 254
 DB 241 CKTEWIEKTQVAS 254
 RESULT 7
 ABP54360
 ID ABP54360 standard; protein; 254 AA.
 XX
 AC ABP54360;
 XX
 DT 20-JAN-2003 (first entry)
 DE Human KLK4 protein SEQ ID NO:13.
 XX
 KW Human; KLK4; cancer; benign tumour; cytostatic4.
 XX
 OS Homo sapiens.
 XX
 XX WO200277243-A1.
 XX
 XX 03-OCT-2002.
 XX
 XX 27-MAR-2002; 2002WO-AU000378.
 XX
 XX 27-MAR-2001; 2001AU-00004022.
 XX
 XX (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
 XX
 XX Dong Y, Clements JA;
 XX
 XX WPI; 2003-029939/02.
 XX
 XX N-PSDB; ABQ83347.
 XX
 XX Detecting the presence or diagnosing the risk of cancer or benign tumor,
 PT e.g. an ovarian, endometrial or prostate cancer, by determining the
 PT presence of or detecting aberrant expression of KLK4 in a biological

PT sample from the patient.
 XX
 XX Disclosure; Page 118-119; 126pp; English.
 XX
 CC The present invention describes a method (M1) for detecting the presence
 CC or diagnosing the risk of cancer or benign tumour in a patient. M1
 CC comprises determining the presence of or detecting aberrant expression of
 CC KLK4 in a biological sample obtained from the patient. KLK4 has
 CC cytostatic activity. The method is useful for detecting the presence or
 CC diagnosing the risk of a cancer or a benign tumour in a patient,
 CC particularly an ovarian, endometrial or prostate cancer, or a cancer or
 CC benign tumour associated with an organ or tissue from the ovaries, or
 CC endometrium or prostate. An agent which can be used for restoring or
 CC modulating KLK4 expression can be used for treating or preventing cancer
 CC or benign tumour. KLK4 polynucleotides, polypeptides or antigen-binding
 CC molecules from the present invention can be used for detecting aberrant
 CC KLK4 polynucleotides or aberrant K4 polypeptides that correlate with a
 CC cancer or a benign tumour. The present sequence represents human KLK4
 CC from the present invention
 XX
 SQ Sequence 254 AA;
 Query Match 100.0%; Score 1369; DB 6; Length 254;
 Best Local Similarity 100.0%; Pred. No. 8.6e-96;
 Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MATAGNPWGFWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWQAALVMENELFCGVL 60
 DB 1 MATAGNPWGFWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWQAALVMENELFCGVL 60
 QY 61 VHPQWVLSAAHCFQNSYTTIGLHLSLEADQEPGSMVEASLSVRHPEYRPLLANDMLI 120
 DB 61 VHPQWVLSAAHCFQNSYTTIGLHLSLEADQEPGSMVEASLSVRHPEYRPLLANDMLI 120
 QY 121 KLDESSESDDTIRSIASQCTAGNSCLVSGWGLLANGRMPTVLCVNVSVSEVCSK 180
 DB 121 KLDESSESDDTIRSIASQCTAGNSCLVSGWGLLANGRMPTVLCVNVSVSEVCSK 180
 QY 181 LYDPLYPHPSMFCAGGGQDQKDSNGDSGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
 DB 181 LYDPLYPHPSMFCAGGGQDQKDSNGDSGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
 QY 241 CKTEWIEKTQVAS 254
 DB 241 CKTEWIEKTQVAS 254
 RESULT 8
 ABP54357
 ID ABP54357 standard; protein; 254 AA.
 XX
 AC ABP54357;
 XX
 DT 20-JAN-2003 (first entry)
 DE Human KLK4 protein SEQ ID NO:6.
 XX
 KW Human; KLK4; cancer; benign tumour; cytostatic.
 XX
 OS Homo sapiens.
 XX
 XX WO200277243-A1.
 XX
 XX 03-OCT-2002.
 XX
 XX 27-MAR-2002; 2002WO-AU000378.
 XX
 XX 27-MAR-2001; 2001AU-00004022.
 XX
 XX (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
 XX
 XX Dong Y, Clements JA;
 PI

DR WPI: 2003-029939/02.
DR N-PSDB; ABQ83343.
XX
PT Detecting the presence or diagnosing the risk of cancer or benign tumor,
PT e.g. an ovarian, endometrial or prostate cancer, by determining the
PT presence of or detecting aberrant expression of KLK4 in a biological
PT sample from the patient.
XX
PS Disclosure; Fig 3; 126pp; English.
XX
CC The present invention describes a method (M1) for detecting the presence
CC or diagnosing the risk of cancer or benign tumour in a patient. M1
CC comprises determining the presence of or detecting aberrant expression of
CC KLK4 in a biological sample obtained from the patient. KLK4 has
CC cytostatic activity. The method is useful for detecting the presence or
CC diagnosing the risk of a cancer or a benign tumour in a patient,
CC particularly an ovarian, endometrial or prostate cancer, or a cancer or
CC benign tumour associated with an organ or tissue from the ovaries,
CC endometrium or prostate. An agent which can be used for restoring or
CC modulating KLK4 expression can be used for treating or preventing cancer
CC or benign tumour. KLK4 polynucleotides, polypeptides or antigen-binding
CC molecules from the present invention can be used for detecting aberrant
CC KLK4 polynucleotides or aberrant K4 polypeptides that correlate with a
CC cancer or a benign tumour. The present sequence represents human KLK4
CC from the present invention
XX
SQ Sequence 254 AA;

Query Match 100.0%; Score 1369; DB 6; Length 254;
Best Local Similarity 100.0%; Pred. No. 8.6e-96;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATAGNPGWFLGYLLIGVAGSLVSGSCQIINGEDCSPHSQPQQAALVMENELFCSGVL 60
Db 1 MATAGNPGWFLGYLLIGVAGSLVSGSCQIINGEDCSPHSQPQQAALVMENELFCSGVL 60

QY 61 VHPQWVLSAAHCFQNSYTTIGLHLSLEADQEPGSMVEASLSVRHPEYRNPRLANDLMLI 120
Db 61 VHPQWVLSAAHCFQNSYTTIGLHLSLEADQEPGSMVEASLSVRHPEYRNPRLANDLMLI 120

QY 121 KLDESVSSEDTRISISASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
Db 121 KLDESVSSEDTRISISASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180

QY 181 LYDPLYPHSMFCAGGQDQKSCNGDSGGPLICNGYLQGLVSGKAPCGGVPGVYTNL 240
Db 181 LYDPLYPHSMFCAGGQDQKSCNGDSGGPLICNGYLQGLVSGKAPCGGVPGVYTNL 240

QY 241 CKFTWIEKTVQAS 254
Db 241 CKFTWIEKTVQAS 254

RESULT 9
ID ABR54391 standard; protein; 254 AA.
XX
AC ABR54391;
XX
DT 28-AUG-2003 (first entry)
XX
DE Prostate tumour specific protein sequence SEQ ID 525.
XX
KW Cytostatic; gene therapy; prostate-specific protein; PSP; human;
KW immune response; prostate cancer.
XX
OS Homo sapiens.
XX
PN W0200289747-A2.
XX
PD 14-NOV-2002.
XX
PF 09-MAY-2002; 2002WO-US014753.

XX 09-MAY-2001; 2001US-00852911.
PR 29-JUN-2001; 2001US-00895814.
PR 10-DEC-2001; 2001US-00012896.
PA (CORI-) CORIXA CORP.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
PI Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
PI McNeill PD, Houghton RL, Vinals Y De BassolsC, Foy TM, Watanabe Y;
PI Deng T;
XX
XX WPI; 2003-167130/16.
XX
XX New prostate-specific proteins and genes, useful in gene therapy,
XX particularly for stimulating an immune response in a patient, or treating
XX prostate cancer in a patient, as well as for diagnosing prostate cancer
XX in a patient.
XX
XX Example 3; Page 472; 691pp; English.
XX
XX The present invention relates to novel prostate-specific proteins (PSP)
XX and their coding sequences. The PSPs and their coding sequences are
XX useful for stimulating an immune response in a patient, or for treating
XX prostate cancer in a patient and for determining, detecting or diagnosing
XX the presence of a cancer in a patient. The present sequence was used to
XX illustrate the invention
XX
SQ Sequence 254 AA;

Query Match 100.0%; Score 1369; DB 6; Length 254;
Best Local Similarity 100.0%; Pred. No. 8.6e-96;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATAGNPGWFLGYLLIGVAGSLVSGSCQIINGEDCSPHSQPQQAALVMENELFCSGVL 60
Db 1 MATAGNPGWFLGYLLIGVAGSLVSGSCQIINGEDCSPHSQPQQAALVMENELFCSGVL 60

QY 61 VHPQWVLSAAHCFQNSYTTIGLHLSLEADQEPGSMVEASLSVRHPEYRNPRLANDLMLI 120
Db 61 VHPQWVLSAAHCFQNSYTTIGLHLSLEADQEPGSMVEASLSVRHPEYRNPRLANDLMLI 120

QY 121 KLDESVSSEDTRISISASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
Db 121 KLDESVSSEDTRISISASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180

QY 181 LYDPLYPHSMFCAGGQDQKSCNGDSGGPLICNGYLQGLVSGKAPCGGVPGVYTNL 240
Db 181 LYDPLYPHSMFCAGGQDQKSCNGDSGGPLICNGYLQGLVSGKAPCGGVPGVYTNL 240

QY 241 CKFTWIEKTVQAS 254
Db 241 CKFTWIEKTVQAS 254

RESULT 10
ID ABR13975 standard; protein; 254 AA.
XX
AC ABR13975;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human prostate specific protein P703P.
XX
KW Human; prostate specific cDNA; cytostatic; immunostimulant; gene therapy;
KW cell therapy; vaccine; T-cell epitope;
KW class I major histocompatibility complex allele; MHC; prostate cancer;
KW tumour; antigen presenting cell.
XX
OS Homo sapiens.
XX

PN US2003185830-A1.
 XX 02-OCT-2003.
 XX 12-NOV-2002; 2002US-00294025.
 XX 25-FEB-1997; 97US-00806099.
 PR 01-AUG-1997; 97US-00904804.
 PR 09-FEB-1998; 98US-00020956.
 PR 25-FEB-1998; 98US-00030607.
 PR 14-JUL-1998; 98US-00115453.
 PR 23-SEP-1998; 98US-00159812.
 PR 15-JAN-1999; 99US-00232149.
 PR 09-APR-1999; 99US-00288946.
 PR 13-JUL-1999; 99US-00352616.
 PR 12-NOV-1999; 99US-00439313.
 PR 18-NOV-1999; 99US-00443686.
 PR 14-JAN-2000; 2000US-00483672.
 PR 27-MAR-2000; 2000US-00536857.
 PR 09-MAY-2000; 2000US-00568100.
 PR 12-MAY-2000; 2000US-00570737.
 PR 13-JUN-2000; 2000US-00593793.
 PR 27-JUN-2000; 2000US-00605783.
 PR 09-AUG-2000; 2000US-00636215.
 PR 29-AUG-2000; 2000US-00651236.
 PR 06-SEP-2000; 2000US-00657279.
 PR 10-OCT-2000; 2000US-00679426.
 PR 02-SEP-2000; 2000US-00685166.
 PR 09-NOV-2000; 2000US-00709729.
 PR 12-JAN-2001; 2001US-00759143.
 PR 09-FEB-2001; 2001US-00780669.
 PR 09-MAY-2001; 2001US-00852911.
 PR 29-JUN-2001; 2001US-00895814.
 PR 10-DEC-2001; 2001US-00012896.
 PR 09-MAY-2002; 2002US-00144678.
 XX (CORI-) CORIXA CORP.
 XX
 PI Xu J, Stolk JA, Kalos MD;
 XX
 DR WPI; 2003-756193/71.
 DR N-PSDB; ADB13974.
 XX
 PT New isolated polypeptide for use in a vaccine for stimulating an immune
 PT response, or for treating or diagnosis cancer, preferably prostate
 PT cancer.
 XX
 PS Example 3; Page; 101pp; English.
 XX
 CC The invention relates to an isolated polypeptide comprising no more than
 CC 11-542 amino acids of ADB13563 comprising a sequence ADB14487. The
 CC peptides comprise a fragment ADB13563 of that contain naturally processed
 CC T-cell epitopes for 3 class I major histocompatibility complex (MHC)
 CC alleles. ADB13563 is a polypeptide encoded by a human prostate specific
 CC cDNA, one of 648 disclosed as new. Also included are nucleic acids
 CC encoding the proteins and peptides, expression vectors, a host cell
 CC transformed with the vector, an isolated antibody (or antigen binding
 CC fragment) that specifically binds to the protein or peptide, detecting
 CC the presence of a cancer in a patient (comprising contacting a patient
 CC sample with a binding agent that binds to the peptides or a polypeptide
 CC appearing as ADB13558, detecting the amount of polypeptide that binds to
 CC the agent and comparing the amount of polypeptide to a predetermined cut-
 CC off value to determine the presence of cancer), a fusion protein
 CC comprising the peptides or proteins, stimulating or expanding T cells
 CC specific for a tumour protein comprising contacting T cells with the
 CC peptides or the isolated T cell population, treating prostate cancer in a
 CC patient comprising administering a composition comprising the peptides,
 CC nucleic acids, antibodies or compounds, determining the presence of a
 CC cancer in a patient and treating prostate cancer in a patient comprising
 CC incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated
 CC from a patient with the peptides or antigen presenting cells that express
 CC the peptides so that the T cells proliferate, and administering the
 CC proliferated T cells to the patient. The peptides (or an oligonucleotide

CC that hybridises to nucleic acid encoding them), is used to detect the
 CC presence of cancer in a patient. The peptides, nucleic acids encoding, or
 CC antigen-presenting cells expressing the nucleic acid, are used to
 CC stimulate or expand T cells specific for a tumour protein. The peptides,
 CC nucleic acids, antibodies, fusion proteins, T cell populations or antigen
 CC presenting cells are used to stimulate an immune response or treat
 CC prostate cancer in a patient. The present sequence is a prostate specific
 CC protein of the invention. Note: Except where otherwise indicated, the
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from USPTO
 CC at seqdata.uspto.gov/sequence.html?DocID=20030185830.

XX Sequence 254 AA;

Query Match 100.0%; Score 1369; DB 7; Length 254;
 Best Local Similarity 100.0%; Pred. No. 8.6e-96;
 Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MATAGNPGWFLGYLILGVAGSLVSGSCSIINGEDCSPHSQPWAALVMENELFCSGVL 60
 DB 1 MATAGNPGWFLGYLILGVAGSLVSGSCSIINGEDCSPHSQPWAALVMENELFCSGVL 60
 QY 61 VHPQWVLSAAHCFQNSYTIIGLHLSLEADQEPGSMVEASLSVRHPEYRPLANDLMLI 120
 DB 61 VHPQWVLSAAHCFQNSYTIIGLHLSLEADQEPGSMVEASLSVRHPEYRPLANDLMLI 120
 QY 121 KLDSESVESDITRSISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
 DB 121 KLDSESVESDITRSISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
 QY 181 LYDPLYHPSMFCAGGQDQKDCSCNGDSGGPLICNGYLOGLVSFKGAPCGQGVGVYTNL 240
 DB 181 LYDPLYHPSMFCAGGQDQKDCSCNGDSGGPLICNGYLOGLVSFKGAPCGQGVGVYTNL 240
 QY 241 CKFTIEWIEKTVQAS 254
 DB 241 CKFTIEWIEKTVQAS 254

RESULT 11

ADG26391
 ID ADG26391 standard; protein; 254 AA.
 XX AC ADG26391;
 XX 26-FEB-2004 (first entry)
 XX Human prostate-specific polypeptide #60.
 DE Human; prostate-specific polypeptide; prostate cancer; cytostatic.
 KW Homo sapiens.
 OS US2003157089-A1.
 XX 21-AUG-2003.
 PD 09-MAY-2002; 2002US-00144678.
 XX 25-FEB-1997; 97US-00806099.
 PR 01-AUG-1997; 97US-00904804.
 PR 09-FEB-1998; 98US-00020956.
 PR 25-FEB-1998; 98US-00030607.
 PR 14-JUL-1998; 98US-00115453.
 PR 23-SEP-1998; 98US-00159812.
 PR 15-JAN-1999; 99US-00232149.
 PR 09-APR-1999; 99US-00288946.
 PR 13-JUL-1999; 99US-00352616.
 PR 12-NOV-1999; 99US-00439313.
 PR 18-NOV-1999; 99US-00443686.
 PR 14-JAN-2000; 2000US-00483672.
 PR 27-MAR-2000; 2000US-00536857.
 PR 09-MAY-2000; 2000US-00568100.

PR 12-MAY-2000; 2000US-00570737.
 PR 13-JUN-2000; 2000US-00593793.
 PR 27-JUN-2000; 2000US-00605783.
 PR 09-AUG-2000; 2000US-00636215.
 PR 29-AUG-2000; 2000US-00651236.
 PR 06-SEP-2000; 2000US-00657279.
 PR 02-OCT-2000; 2000US-00679426.
 PR 10-OCT-2000; 2000US-00685166.
 PR 09-NOV-2000; 2000US-00709729.
 PR 12-JAN-2001; 2000US-00759143.
 PR 09-FEB-2001; 2000US-00780669.
 PR 09-MAY-2001; 2000US-00852911.
 PR 29-JUN-2001; 2000US-00895814.
 PR 10-DEC-2001; 2000US-00012896.
 XX

PA (CORI-) CORIXA CORP.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
 PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
 PI Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
 PI McNeill PD, Houghton RL, Vinals Y De BassolsC, Foy TM, Watanabe Y;
 PI Meagher MJ, Deng T;
 XX

WPI; 2003-777973/73.
 DR N-PSDB; ADG26390.

XX New polynucleotides encoding prostate specific polypeptides isolated from
 PT a human prostate tumor cDNA library are useful to diagnose and treat
 PT cancer particularly prostate cancer.

PS Example 3; SEQ ID NO 525; 99pp; English.

XX The invention relates to human prostate-specific polypeptides and the
 CC polynucleotides encoding them. The invention also relates to an isolated
 CC antibody or its antigen-binding fragment that specifically binds a
 CC polypeptide of the invention, a method of detecting cancer in a patient
 CC comprising contacting a biological sample of the patient with an agent
 CC that binds a prostate-specific polypeptide and comparing the amount of
 CC bound polypeptide compared to a predetermined cut-off value and a fusion
 CC protein comprising a prostate-specific polypeptide. The sequences of the
 CC invention are used to diagnose and treat cancer, particularly prostate
 CC cancer. This sequence represents a human prostate-specific polypeptide of
 CC the invention. Note: The sequence data for this patent did not form part
 CC of the printed specification but was obtained in electronic format
 CC directly from USPTO at seqdata.uspto.gov/sequence.html.
 XX

SQ Sequence 254 AA;

Query Match	100.0%;	Score 1369;	DB 7;	Length 254;
Best Local Similarity	100.0%;	Pred. No. 8.6e-96;		
Matches	254;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;

QY	1	MATAGNPGWFLGYLILGVAGSLVSGSCSQIINGDCSPHSQPWQAALVMENELFCSGVL	60
DB	1	MATAGNPGWFLGYLILGVAGSLVSGSCSQIINGDCSPHSQPWQAALVMENELFCSGVL	60
QY	61	VHPQWLAAHCFQNSYTIIGLHLSLEADQEPGSMVEASLSVRHPEYRPLANDLMLI	120
DB	61	VHPQWLAAHCFQNSYTIIGLHLSLEADQEPGSMVEASLSVRHPEYRPLANDLMLI	120
QY	121	KLDESSESDDTIRSIASQCPTAGNSCLVSGWGLLANGMPRTLQCVNVSVVSEVCSK	180
DB	121	KLDESSESDDTIRSIASQCPTAGNSCLVSGWGLLANGMPRTLQCVNVSVVSEVCSK	180
QY	181	LYDPLYPHSMFCAGGQDQKDCNCGDSGGPLICNGYLOGLVSGFKAPCGQGVPGVYTNL	240
DB	181	LYDPLYPHSMFCAGGQDQKDCNCGDSGGPLICNGYLOGLVSGFKAPCGQGVPGVYTNL	240
QY	241	CKPTEWIEKTVQAS	254
DB	241	CKPTEWIEKTVQAS	254

RESULT 12
 AAB74830

ID AAB74830 standard; protein; 1079 AA.

XX AAB74830;

DT 14-JUN-2001 (first entry)

DE Prostate tumour antigen amino acid sequence for a fusion protein.

XX Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;
 KW prostate cancer; immunogenic; cytostatic; vaccine.

OS Homo sapiens.

PN WO200125272-A2.

PD 12-APR-2001.

PF 04-OCT-2000; 2000WO-US027464.

PR 04-OCT-1999; 99US-0157455P.

PA (CORI-) CORIXA CORP.

PI Xu J, Skeiky YAW, Reed SG, Cheever MA;

DR WPI; 2001-245062/25.

PT Prostate specific protein and its encoding polynucleotide, useful for the
 PT treatment and diagnosis of prostate cancer.

PS Disclosure; Page 272-276; 276pp; English.

XX The present invention describes an isolated polypeptide (I) comprising at
 CC least an immunogenic portion of a prostate tumour antigen protein or its
 CC variant. (I) have cytostatic activity and can be used in vaccine
 CC production. (I), prostate tumour antigen polynucleotides, an antigen
 CC presenting cell (APC e.g. a dendritic cell) that expresses (I), and a
 CC pharmaceutical composition containing (I) are useful for inhibiting the
 CC development of cancer in a patient. Antibodies specific for prostate
 CC specific proteins and oligonucleotides that hybridise to a polynucleotide
 CC that encodes a prostate specific protein are useful for detecting the
 CC presence or absence of a cancer or monitoring the progression the
 CC progression of a cancer, especially prostate cancer. AAH02422 to AAH2872,
 CC AAB74798 to AAB74821 and AAB74830 are sequences used in the
 CC exemplification of the present invention

SQ Sequence 1079 AA;

Query Match	100.0%;	Score 1369;	DB 4;	Length 1079;
Best Local Similarity	100.0%;	Pred. No. 3.7e-95;		
Matches	254;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;

QY	1	MATAGNPGWFLGYLILGVAGSLVSGSCSQIINGDCSPHSQPWQAALVMENELFCSGVL	60
DB	271	MATAGNPGWFLGYLILGVAGSLVSGSCSQIINGDCSPHSQPWQAALVMENELFCSGVL	330
QY	61	VHPQWLAAHCFQNSYTIIGLHLSLEADQEPGSMVEASLSVRHPEYRPLANDLMLI	120
DB	331	VHPQWLAAHCFQNSYTIIGLHLSLEADQEPGSMVEASLSVRHPEYRPLANDLMLI	390
QY	121	KLDESSESDDTIRSIASQCPTAGNSCLVSGWGLLANGMPRTLQCVNVSVVSEVCSK	180
DB	391	KLDESSESDDTIRSIASQCPTAGNSCLVSGWGLLANGMPRTLQCVNVSVVSEVCSK	450
QY	181	LYDPLYPHSMFCAGGQDQKDCNCGDSGGPLICNGYLOGLVSGFKAPCGQGVPGVYTNL	240
DB	451	LYDPLYPHSMFCAGGQDQKDCNCGDSGGPLICNGYLOGLVSGFKAPCGQGVPGVYTNL	510
QY	241	CKPTEWIEKTVQAS	254
DB	511	CKPTEWIEKTVQAS	524

RESULT 13

ABU71860
ID ABU71860 standard; protein; 1079 AA.

XX AC ABU71860;

XX DT 10-JUN-2003 (first entry)

XX Prostate specific antigen fusion protein #2.
XX Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
KW immunogen; cancer; prostate specific antigen; PSA;
KW prostatic acid phosphatase; PAP; prostate specific membrane antigen;
KW PSMA.

XX Homo sapiens.

OS Synthetic.

XX US2002192763-A1.

XX 19-DEC-2002.

XX 29-JUN-2001; 2001US-00895793.

XX 04-OCT-1999; 99US-0157455P.

PR 04-OCT-2000; 2000US-00679272.

PR 28-MAR-2001; 2001US-00822827.

XX (XUJ1) XU J.

PA (DILL) DILLON D C.

PA (MITC) MITCHAM J L.

PA (HARL) HARLOCKER S L.

PA (JIAN) JIANG Y.

PA (KALO) KALOS M D.

PA (FANG) FANGER G R.

PA (RETT) RETTER M W.

PA (STOL) STOLK J A.

PA (DAYC) DAY C H.

PA (VEDV) VEDVICK T S.

PA (CART) CARTER D.

PA (LISX) LI S X.

PA (WANG) WANG A.

PA (SKEI) SKEIKY Y A W.

PA (HEPL) HEPLER W T.

PA (HEND) HENDERSON R A.

PA (HURA) HURAL J P D.

PA (MCNE) MCNEILL P D.

PA (HOUG) HOUGHTON R L.

PA (DBAS) Y DE BASSOLS C V.

PA (FOYT) FOY T M.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;

PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;

PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J;

PI McNeill PD, Houghton RL, Y De Bassols CV, Foy TM;

XX WPI; 2001-245062/25.

DR Prostate specific protein and its encoding polynucleotide, useful for the

XX treatment and diagnosis of prostate cancer.

XX Claim 5; SEQ ID NO 947; 85pp; English.

XX The invention describes a fusion protein comprising at least one amino

CC acid sequence of immunogenic portions of any of the 3 sequences not

CC defined in the specification, or sequences having at least 70 or 90 %

CC sequence identity to any one of the 35 sequences defined in the USPTO web

CC site, which is encoded by any of the 4 nucleotide sequences not defined

CC in the specification. The fusion protein, composition and methods are

CC useful for diagnosing, preventing and/or treating cancer, particularly

CC prostate cancer. The proteins are useful as markers to indicate the

CC presence or absence of cancer. This is the amino acid sequence of a
CC fusion protein of the invention created from fragments of prostate
CC specific antigen (PSA), prostatic acid phosphatase (PAP), prostatic
CC specific membrane antigen (PSMA) and prostate specific antigens of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from the US patent office at
CC seqdata.uspto.gov/sequence.html?DocID=US20020192763
XX

SQ Sequence 1079 AA;

Query Match 100.0%; Score 1369; DB 4; Length 1079;

Best Local Similarity 100.0%; Pred. No. 3.7e-95; Indels 0; Gaps 0;

Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATAGNPGWFLGYLILGVAGSLVSGSCSIINGEDCSPHSQPQAAALVMENELFCSGVL 60

DB 271 MATAGNPGWFLGYLILGVAGSLVSGSCSIINGEDCSPHSQPQAAALVMENELFCSGVL 330

QY 61 VHPQWVLSAHCQFNSYITIGLHSLQADQEPGQVSEASLSVRHPEYNRPLLANDMLI 120

DB 331 VHPQWVLSAHCQFNSYITIGLHSLQADQEPGQVSEASLSVRHPEYNRPLLANDMLI 390

QY 121 KLDESVSSEDTIRSIASQCTAGNSCLVSGWGLLANGRMPTVLQCVNVSVSEVCSK 180

DB 391 KLDESVSSEDTIRSIASQCTAGNSCLVSGWGLLANGRMPTVLQCVNVSVSEVCSK 450

QY 181 LYDPLYHPSMFCAGGQDQKSCNGSGPLICNGYLGVSFGKAPCGQGVPGVYTNL 240

DB 451 LYDPLYHPSMFCAGGQDQKSCNGSGPLICNGYLGVSFGKAPCGQGVPGVYTNL 510

QY 241 CKFTWIEKTVQAS 254

DB 511 CKFTWIEKTVQAS 524

RESULT 14

AAB21320

ID AAB21320 standard; protein; 254 AA.

XX AC AAB21320;

XX DT 02-FEB-2001 (first entry)

XX Human prostate.

XX Human; KLK-L1; KLK-L2; KLK-L3; KLK-L4; KLK-L5; KLK-L6; prostate;

XX kallikrein-like protein; serine protease; cytostatic; cancer;

XX prostrate cancer.

XX Homo sapiens.

XX WO200053776-A2.

XX 14-SEP-2000.

XX 09-MAR-2000; 2000WO-CA000258.

XX 11-MAR-1999; 99US-0124260P.

XX 01-APR-1999; 99US-0127386P.

XX 21-JUL-1999; 99US-0144919P.

XX (MOUN) MOUNT SINAI HOSPITAL.

XX Yousef GM, Diamandis EP;

XX WPI; 2000-587440/55.

XX New kallikrein-like (KLK-L) proteins for diagnosing and treating KLK-L

XX protein mediated disorders, especially cancer.

XX Example 4; Fig 17; 184pp; English.

CC The present sequence is human prostate, a member of the serine protease
CC family. Kallikreins and kallikrein-like proteins are a subgroup of the
CC serine protease enzyme family. They catalyze the selective cleavage of
CC specific polypeptide precursors to release peptides with potent
CC biological activity. Nucleic acids encoding kallikrein-like proteins KUK-
CC L1, KUK-L2, KUK-L3, KUK-L4, KUK-L5 and KUK-L6 have been isolated. The
CC proteins are useful in the treatment, monitoring and diagnosis of
CC cancers, especially prostate cancer. They can also be used to identify a
CC substance that can associate with or mediate the biological activity of
CC the proteins. Antibodies can be used to treat conditions mediated by the
CC kallikrein-like proteins
XX
SQ Sequence 254 AA;

Query Match 99.6%; Score 1364; DB 3; Length 254;
Best Local Similarity 99.6%; Pred. No. 2.1e-95;
Matches 253; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MATAGNPGWFLGYLLGVAGSLVSGSCSIINGEDCSPHSQPQWQAALVMENELFCSGVL 60
DB 1 MATAGNPGWFLGYLLGVAGSLVSGSCSIINGEDCSPHSQPQWQAALVMENELFCSGVL 60
QY 61 VHPQWVLSAAHCFQNSYITIGLHLSLEADQEPGQWVEASLSVRHPEYRPLANDMLI 120
DB 61 VHPQWVLSAAHCFQNSYITIGLHLSLEADQEPGQWVEASLSVRHPEYRPLANDMLI 120
QY 121 KLDESVSSEDRTIRSIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVSEVCSK 180
DB 121 KLDESVSSEDRTIRSIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVSEVCSK 180
QY 181 LYDPLYHPSMFCAGGQDQKDCNCGDGGPLICNGYLGVSFGKAPCGQGVPGVYTNL 240
DB 181 LYDPLYHPSMFCAGGQDQKDCNCGDGGPLICNGYLGVSFGKAPCGQGVPGVYTNL 240
QY 241 CKFTWIEKTVQAS 254
DB 241 CKFTWIEKTVQAS 254

RESULT 15

AA72525
ID AA72525 standard; protein; 254 AA.

AC AA72525;

DT 02-MAY-2001 (first entry)

XX Human prostate antigen #3.

XX Human; prostate; p703p; gene therapy; prostate cancer; cytostatic; PIN;
KW prostate intraepithelial neoplasia; NSI; non-structural protein; vaccine;
KW haemagglutinin; prostatic hyperplasia; prostate-specific serine protease;
XX therapy.

OS Homo sapiens.

XX WO200104143-A2.

XX 18-JAN-2001.

XX 11-JUL-2000; 2000WO-EF006618.

XX 13-JUL-1999; 99US-00352616.

XX 12-NOV-1999; 99US-00439313.

XX 18-NOV-1999; 99US-0043686.

XX 14-JAN-2000; 2000US-00483672.

XX 27-MAR-2000; 2000US-00536857.

XX 09-MAY-2000; 2000US-00568100.

XX 12-MAY-2000; 2000US-00570737.

XX 13-JUN-2000; 2000US-00593793.

XX 27-JUN-2000; 2000GB-00015747.

PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
PA (CORI-) CORIXA CORP.

XX Cabezon Silva T, Dillon DC;

XX WPI; 2001-159380/16.

XX New prostate protein or its fragment linked to a immunological/expression
PT enhancer fusion partner, useful for preparing vaccines for treating
PT prostate cancers or prostate associated tumors.

XX Claim 2; Page 49; 50pp; English.

XX The present protein sequence is a human prostate antigen. The invention
CC relates to a prostate protein (prostate-specific serine protease) or its
CC fragment fused to an immunological or an expression enhancer fusion
CC partner, such as NSI (haemagglutinin). The fusion protein is used for
CC formulating vaccines useful for immunotherapeutically treating patients
CC susceptible to or suffering from prostate-cancer and prostate-expressing
CC tumours other than prostate tumours, prostatic hyperplasia and prostate
CC intraepithelial neoplasia (PIN). Genetic constructs containing prostate
CC nucleic acids are also useful in gene therapy techniques to induce an
CC immune response
XX

SQ Sequence 254 AA;

Query Match 99.6%; Score 1364; DB 4; Length 254;
Best Local Similarity 99.6%; Pred. No. 2.1e-95;
Matches 253; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATAGNPGWFLGYLLGVAGSLVSGSCSIINGEDCSPHSQPQWQAALVMENELFCSGVL 60
DB 1 MATAGNPGWFLGYLLGVAGSLVSGSCSIINGEDCSPHSQPQWQAALVMENELFCSGVL 60

QY 61 VHPQWVLSAAHCFQNSYITIGLHLSLEADQEPGQWVEASLSVRHPEYRPLANDMLI 120
DB 61 VHPQWVLSAAHCFQNSYITIGLHLSLEADQEPGQWVEASLSVRHPEYRPLANDMLI 120

QY 121 KLDESVSSEDRTIRSIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVSEVCSK 180
DB 121 KLDESVSSEDRTIRSIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVSEVCSK 180

QY 181 LYDPLYHPSMFCAGGQDQKDCNCGDGGPLICNGYLGVSFGKAPCGQGVPGVYTNL 240
DB 181 LYDPLYHPSMFCAGGQDQKDCNCGDGGPLICNGYLGVSFGKAPCGQGVPGVYTNL 240

QY 241 CKFTWIEKTVQAS 254

DB 241 CKFTWIEKTVQAS 254

Search completed: February 10, 2005, 08:51:13
Job time : 167 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2005, 08:37:40 ; Search time 177 Seconds
(without alignments)
734.848 Million cell updates/sec

Title: US-09-895-814-525
Perfect score: 1369
Sequence: 1 MATAGNPMGWFGLYLILGVA.....GVYTNLCKFTWIKTVQAS 254

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1369	100.0	254	1	KLK4_HUMAN	Q9Y5K2 homo sapien
2	1113	81.3	254	2	Q9XSN6	Q9XSN6 sus scrofa
3	1098	80.2	205	2	Q96JEO	Q96JEO homo sapien
4	1087	79.4	205	2	Q96JED	Q96JED homo sapien
5	1069.5	78.1	204	2	Q96JE1	Q96JE1 homo sapien
6	1010	73.8	255	2	Q9JIS2	Q9JIS2 mus musculus
7	997.5	72.9	256	2	Q6IE12	Q6IE12 rattus norv
8	995	72.7	255	2	Q9ZOM1	Q9ZOM1 mus musculus
9	848	61.9	195	2	Q96PT0	Q96PT0 homo sapien
10	845	61.7	159	2	Q96PT1	Q96PT1 homo sapien
11	675	49.3	131	2	Q96JD8	Q96JD8 homo sapien
12	671	49.0	293	1	KLK5_HUMAN	Q9Y337 homo sapien
13	637.5	46.6	293	2	Q9D140	Q9D140 mus musculus
14	577	42.1	146	2	Q96JD7	Q96JD7 homo sapien
15	575	42.0	269	2	Q8IU55	Q8IU55 homo sapien
16	574	41.9	110	2	Q96RU5	Q96RU5 homo sapien
17	569.5	41.6	260	1	NRPN_RAT	Q88780 rattus norv
18	567.5	41.5	253	1	KLK7_HUMAN	P49862 homo sapien
19	563.5	41.2	260	1	NRPN_MOUSE	Q61955 mus musculus
20	556.5	40.7	253	2	Q8N5N9	Q8N5N9 homo sapien
21	549	40.1	250	1	KLK6_HUMAN	Q9UBX7 homo sapien
22	540.5	39.5	242	2	Q7TIR8	Q7TIR8 pangasius h
23	538.5	39.3	250	2	Q8CGR5	Q8CGR5 mus musculus
24	537.5	39.3	242	2	Q8OV54	Q8OV54 mus musculus
25	537	39.2	276	2	Q8CGR6	Q8CGR6 mus musculus
26	535.5	39.1	251	1	KLK6_HUMAN	Q9PG33 homo sapien
27	534	39.0	246	2	Q6P3Z0	Q6P3Z0 mus musculus
28	533.5	39.0	251	2	Q6B089	Q6B089 homo sapien
29	529.5	38.7	275	2	Q8IXD7	Q8IXD7 homo sapien
30	529	38.6	249	2	Q91VE3	Q91VE3 m thymopsin
31	527	38.5	250	2	Q63ZF2	Q63ZF2 rattus norv

32	524	38.3	249	2	Q9QYN4	Q9QYN4 mus musculus
33	524	38.3	261	2	Q29474	Q29474 canis famil
34	524	38.3	276	2	Q9QYN3	Q9QYN3 m hippostas
35	519	37.9	249	2	Q788V0	Q788V0 dissostichu
36	517.5	37.8	277	1	KLKD_HUMAN	Q9UKR3 homo sapien
37	517	37.8	247	2	Q9CPN9	Q9CPN9 m mus muscu
38	516	37.7	235	2	Q63274	Q63274 rattus norv
39	515.5	37.7	260	1	KLK8_HUMAN	Q60259 homo sapien
40	515	37.6	244	1	KLKA_RAT	P36375 homo sapien
41	515	37.6	249	2	Q92046	Q92046 dissostichu
42	513.5	37.5	260	2	Q8IW69	Q8IW69 homo sapien
43	512	37.4	239	2	Q63275	Q63275 rattus norv
44	510.5	37.3	248	1	TRY3_CHICK	Q90629 gallus gall
45	509	37.2	261	1	KLK3_MOUSE	P00756 mus musculus

ALIGNMENTS

RESULT 1	KLK4_HUMAN	STANDARD	PRT;	254 AA.
ID	Q9Y5K2: Q9CZL6; Q9UBJ6;			
AC	16-OCT-2001 (Rel. 40, Created)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Kallikrein-1 precursor (EC 3.4.21.-) (protease) (Kallikrein-like protein 1) (KLK-L1) (Enamel matrix serine proteinase 1).			
DE	Name: KLK4; Synonyms: EMSPI, PRSS17, PSTS;			
GN	Homo sapiens (Human).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]_TaxID=9606;			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99179024; PubMed=10077646; DOI=10.1073/pnas.96.6.3114;			
RA	Nelson P.S., Gan L., Ferguson C., Moss P., Gellinas R., Hood L.,			
RT	Wang K.;			
RT	"Molecular cloning and characterization of prostate, an androgen-regulated serine protease with prostate-restricted expression.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 96:3114-3119(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99413477; PubMed=10485467;			
RA	Yousef G.M., Obiezu C.V., Loh L., Black M.H., Diamandis E.P.;			
RT	"Prostate/KLK-L1 is a new member of the human kallikrein gene family, is expressed in prostate and breast tissues, and is hormonally regulated.";			
RL	Cancer Res. 59:4252-4256(1999).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99367447; PubMed=10438493; DOI=10.1074/jbc.274.33.23210;			
RA	Stephenson S.A., Verit A., Ashworth L.K., Clements J.A.;			
RT	"Localization of a new prostate-specific antigen-related serine protease gene, KLK4, is evidence for an expanded human kallikrein gene family cluster on chromosome 19q13.3-14.4.";			
RL	J. Biol. Chem. 274:23210-23214(1999).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;			
RA	Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,			
RT	Moss P., Paepert B., Wang R.;			
RT	"Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region.";			
RL	Gene 257:119-130(2000).			
RN	[5]			
RP	SEQUENCE FROM N.A., AND CHARACTERIZATION.			
RX	MEDLINE=20323211; PubMed=10891090; DOI=10.1016/S0378-1119(00)00203-1;			
RA	Hu J.-C., Zhang C., Sun X., Yang Y., Cao X., Ryu O., Simmer J.P.;			
RT	"Characterization of the mouse and human PRSS17 genes, their relationship to other serine proteases, and the expression of PRSS17 in developing mouse incisor.";			
RL	Gene 251:1-8(2000).			

[6] SEQUENCE FROM N.A.
 RP TISSUE-Prostatic carcinoma;
 RC Korkmaz K.S., Korkmaz C.G., Saatcioglu F.;
 RA Submitted (APR-2000) to the EMBL/GenBank/DBSJ databases.
 RL
 RP SEQUENCE FROM N.A.
 RX PubMed=15057824; DOI=10.1038/nature02399;
 RA Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,
 RA Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M.,
 RA Aerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E.,
 RA Caenepeel S., Carrano A.V., Caille C., Chan Y.M., Christensen M.,
 RA Cleland C.A., Copeland A., Dallin E., Dehal P., Denys M., Dettler J.C.,
 RA Escobar J., Flowers D., Fotopoulos D., Garcia C., Georgescu A.M.,
 RA Glavina T., Gomez M., Gonzales E., Groza M., Hammon N., Hawkins T.,
 RA Haydu L., Ho I., Huang W., Israni S., Jett J., Kadner K., Kimball H.,
 RA Kobayashi A., Larionov V., Letourneau S., Lopez F., Lou Y., Lowry S.,
 RA Malfatti S., Martinez D., McCreedy P.M., Medina C., Morgan J.,
 RA Nelson K., Nolan M., Ovcharenko I., Pittluck S., Pollard M.,
 RA Popkie A.P., Predki P., Quan G., Ramirez L., Raab S., Retterer J.,
 RA Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,
 RA Slezak T., Solovayev V., Thayer N., Tice H., Tsai M., Ustaszewska A.,
 RA Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I.,
 RA Furey T.S., DeJong P., Dickson M., Gordon D., Eichler E.E.,
 RA Pennacchio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M.,
 RA Rubin E.M., Lucas S.M.;
 RT "The DNA sequence and biological organization of human chromosome 19";
 RA Nature 428:529-535 (2004).
 RP
 RN SEQUENCE OF 22-254 FROM N.A.
 RA Simmer J.P., Ryu O.H., Qian Q., Zhang C., Cao X., Sun X., Hu C.-C.;
 RT "Cloning and characterization of a cDNA encoding human ENSP1.";
 RL (In) Goldberg M. (eds.)
 RL Chemistry and biology of mineralized tissues, pp.1-1, American Academy
 RL of Orthopaedic Surgeons, Vitell (2000).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed in prostate.
 CC -1- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
 CC subfamily.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC entities requires a license agreement. (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AF113140; AAD21580.1; -;
 DR EMBL; AF113141; AAD21581.1; -;
 DR EMBL; AF113142; AAD21582.1; -;
 DR EMBL; AF135023; AAD26424.2; -;
 DR EMBL; AF148532; AAD38019.1; -;
 DR EMBL; AF243527; AAG33357.1; -;
 DR EMBL; AF228497; AAF70620.1; -;
 DR EMBL; AF259969; AAF81227.1; -;
 DR EMBL; AC037199; -; NOT ANNOTATED_CDS.
 DR EMBL; AF126401; AAG43246.1; -;
 DR HSSP; P00760; IEZX.
 DR MEROPS; S01.251; -;
 DR Genew; HGNC:6365; KLIK4.
 DR MIM; 603767; -;
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0008236; F:serine-type peptidase activity; NAS.
 DR GO; GO:0008508; P:proteolysis and peptidolysis; NAS.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR InterPro; IPR001254; Peptidase_S1.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS02400; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.

KW Glycoprotein; Hydrolase; Serine protease; Signal; Zymogen.
 FT SIGNAL 1 26 Potential.
 FT PROPEP 27 30 Potential.
 FT CHAIN 31 254 Kallikrein 4.
 FT ACT_SITE 71 71 Charge relay system (By similarity).
 FT ACT_SITE 116 116 Charge relay system (By similarity).
 FT ACT_SITE 207 207 Charge relay system (By similarity).
 FT DISULFID 37 167 By similarity.
 FT DISULFID 56 72 By similarity.
 FT DISULFID 141 241 By similarity.
 FT DISULFID 148 213 By similarity.
 FT DISULFID 178 192 By similarity.
 FT DISULFID 203 228 By similarity.
 FT CARBOHYD 169 169 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 197 197 Q -> H (in Ref. 1 and 4).
 SQ SEQUENCE 254 AA; 27022 MW; 9C475E22B6EE0CB8 CRC64;
 Query Match 100.0%; Score 1369; DB 1; Length 254;
 Best Local Similarity 100.0%; Pred. No. 2.5e-113;
 Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MATAGNPGWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPQWQALVMEELFCGVL 60
 DB 1 MATAGNPGWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPQWQALVMEELFCGVL 60
 QY 61 VHPQWVLSAAHCFQNSYITIGLHLSLEADQBPQSGQVVEASLSVRHPEYRNPRLANDMLI 120
 DB 61 VHPQWVLSAAHCFQNSYITIGLHLSLEADQBPQSGQVVEASLSVRHPEYRNPRLANDMLI 120
 QY 121 KLDVSVSSDTRISIRSIASQCPAGNSCLVSGWGLLANGMPVLCVNVSVSVSEVCSK 180
 DB 121 KLDVSVSSDTRISIRSIASQCPAGNSCLVSGWGLLANGMPVLCVNVSVSVSEVCSK 180
 QY 181 LYDPLYHPSMFCAGGQDQKSCNDSGGLICNGYLOGLVSGKAPCGQGVGVYTNL 240
 DB 181 LYDPLYHPSMFCAGGQDQKSCNDSGGLICNGYLOGLVSGKAPCGQGVGVYTNL 240
 QY 241 CKFTIEWIEKTVQAS 254
 DB 241 CKFTIEWIEKTVQAS 254
 RESULT 2
 QXSN6 PRELIMINARY; PRT; 254 AA.
 AC QXSN6;
 DT 01-NOV-1999 (TREMELrel. 12, Created)
 DT 01-NOV-1999 (TREMELrel. 12, Last sequence update)
 DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
 DE Enamel matrix serine proteinase 1 precursor.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98126310; PubMed=9465170;
 RA Simmer J.P., Fukae M., Tanabe T., Yamakoshi Y., Uchida T., Xue J.,
 RA Margolis H.C., Shimizu M., Dehart B.C., Hu C.-C., Bartlett J.D.;
 RT "Purification, characterization, and cloning of enamel matrix serine
 RT proteinase 1";
 RL J. Dent. Res. 77:377-386 (1998).
 CC -1- SIMILARITY: Belongs to peptidase family S1.
 DR EMBL; U76256; AAB94638.1; -;
 DR HSSP; P00760; IEZX.
 DR MEROPS; S01.251; -;
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR00134; Peptidase_S1.
 DR InterPro; IPR009003; Pept_Ser_Cys.

RESULT 4	
Q96JEU	
Q96JEU	
ID	PRELIMINARY; PRT; 205 AA.
Q96JEU	
AC	Q96JEU
DT	01-DEC-2001 (TEMBLrel. 19, Created)
DT	01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT	01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE	ARM1.
OS	Homo sapiens (Human).
OC	Chordata; Vertebrata; Euteleostomi;
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OC	Mammalia; Eucnemia; Primates; Catarrhini; Hominoidea; Homo.
OX	NCBI_TaxId=9606;
QY	[1]
RN	SEQUENCE FROM N.A.
RP	TSUCE=Prostate;
RC	MEDLINE=21398046; PubMed=11506707; DOI=10.1089/10454901750361497;
RA	Korkmaz K.S., Korkmaz C.G., Preclow T.G., Saatciloglu F.;
EX	"Distinctly different gene structure of KLU4/KLK-L1/Protease/ARMI
RT	compared with other members of the kallikrein family - Perinuclear
RT	localization, alternative cDNA forms and regulation by multiple
RT	hormones";
RL	DNA Cell Biol. 20:435-445(2001);
CC	-1- SIMILARITY: Belongs to peptidase family S1.
DR	EMBL; AF259964; AAK1700.1; peptidase family S1
DR	HSSP; P00760; 1EZX.
DR	GO; GO:0004263; F:chymotrypsin activity; IEA.
DR	GO; GO:0008233; F:peptidase activity; IEA.
DR	GO; GO:0004295; F:trypsin activity; IEA.
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR	InterPro; IPR001254; Peptidase S1.
DR	InterPro; IPR001131; Peptidase S1A.
DR	InterPro; IPR009003; Pept_Ser_Cys.
DR	Pfam; PF00889; Trypsin; A.
DR	PRINTS; PR00722; CHYMOTRYPSIN.
DR	SMART; SM00020; Tryp_SPC; 1.
DR	PROSITE; PS0240; TRYPSIN_DOM; 1.
DR	PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR	PROSITE; PS00135; TRYPSIN_SER; 1.
KW	Hydrolase; Protease; Serine protease.
SQL	SEQUENCE 205 AA; 22052 MW; 159B61A20D94BD57 CRC64;
	Query Match 79.4%; Score 1087; DB 2; Length 205;
	Best Local Similarity 99.0%; Pred. No. 2.2e-88;
	Matches 203; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	50 MENELFCSGVLVHPQWVLSAAHCFQNSYITIGLGLHSLEADQFGSQMVEASLSVRHPEYN 109
Db	1 MENELFCSGVLVHPQWVLSAAHCFQNYITIGLGLHSLEADQFGSQMVEASLSVRHPEYN 60

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QY 110 RPLANDLMLIKLDESVESDTRISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVN 169
Db 61 RPLANDLMLIKLDESVESDTRISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVN 120

QY 170 VSVSEVCSKLYDPLYPHSMFCAGGQDQKDCSCNGDSGGPLICNGYLQGLVSFGKAPCG 229
Db 121 VSVSEVCSKLYDPLYPHSMFCAGGQDQKDCSCNGDSGGPLICNGYLQGLVSFGKAPCG 180

QY 230 QVGPVGVYTNLCKFTWIEKTVQAS 254
Db 181 QVGPVGVYTNLCKFTWIEKTVQAS 205

RESULT 5
Q96JE1 PRELIMINARY; PRT; 204 AA.
AC Q96JE1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ARM1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=21398046; PubMed=11506707; DOI=10.1089/104454901750361497;
RA Korkmaz K.S., Korkmaz C.G., Pretlow T.G., Saatcioglu F.;
RT "Distinctly different gene structure of KLK4/KLK-Li/Protease/ARM1
RT compared with other members of the kallikrein family - Perinuclear
RT localization, alternative cDNA forms and regulation by multiple
RT hormones.";
RL DNA Cell Biol. 20:435-445 (2001).
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AF259965; AAK71701.1; -.
DR HSP; P00760; LEZK.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
FT SIGNAL
FT CHAIN
SQ SEQUENCE 204 AA; 21811 MW; 45742165D23A53F3 CRC64;

Query Match 78.1%; Score 1069.5; DB 2; Length 204;
Best Local Similarity 98.5%; Pred. No. 7.7e-87;
Matches 202; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 50 MENELFCSGVLVHPQVWLSAAHCFQNSYITIGLHLSLEADQPGSQMVEASLSVRHPEYN 109
Db 1 MENELFCSGVLVHPQVWLSAAHCFQNSYITIGLHLSLEADQPGSQMVEASLSVRHPEYN 60

QY 110 RPLANDLMLIKLDESVESDTRISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVN 169
Db 61 RPLANDLMLIKLDESVESDTRISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVN 119

QY 170 VSVSEVCSKLYDPLYPHSMFCAGGQDQKDCSCNGDSGGPLICNGYLQGLVSFGKAPCG 229
Db 120 VSVSEVCSKLYDPLYPHSMFCAGGQDQKDCSCNGDSGGPLICNGYLQGLVSFGKAPCG 179

QY 230 QVGPVGVYTNLCKFTWIEKTVQAS 254

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Db 180 QVGPVGVYTNLCKFTWIEKTVQAS 204

RESULT 6
Q9JIS2 PRELIMINARY; PRT; 255 AA.
AC Q9JIS2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Enamel matrix serine proteinase 1 precursor.
GN Name=KLK4; Synonyms=Prss17;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=20323211; PubMed=10863090; DOI=10.1016/S0378-1119(00)00203-1;
RA Hu J.C., Zhang C., Sun X., Yang Y., Cao X., Ryu O., Simmer J.P.;
RT "Characterization of the mouse and human PRSS17 genes, their
RT relationship to other serine proteases, and the expression of PRSS17
RT in developing mouse incisors.";
RL Gene 251:1-8(2000).
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AF198031; AAF85937.1; -.
DR HSP; P00760; LEZK.
DR MEROPS; S01.251; -.
DR MGD; MGI:1861379; Klk4.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease; Signal.
FT SIGNAL
FT CHAIN
SQ SEQUENCE 255 AA; 27536 MW; CBF5FBAF7D4D679C CRC64;

Query Match 73.8%; Score 1010; DB 2; Length 255;
Best Local Similarity 70.1%; Pred. No. 1.9e-81;
Matches 178; Conservative 31; Mismatches 45; Indels 0; Gaps 0;

QY 1 MATAGNPGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPQWQAALVMENELFCSGYL 60
Db 2 MYTARTPGWFLGYLILEVTGASASSVSRIIQGDCSPHSQPWQAALFSEDFGFCGVL 61

QY 61 VHPQVWLSAAHCFQNSYITIGLHLSLEADQPGSQMVEASLSVRHPEYNRPLANDLMLI 120
Db 62 VHPQVWLSAAHCFQNSYITIGLHLSLEADQPGSQMVEASLSVRHPEYNRPLANDLMLI 121

QY 121 KLDESVESDTRISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVSEVCSK 180
Db 122 KUNESVIESNTIRSPVATQCPDPTDCLVSGWGLKNGKLPISLQCVNLVASETCRL 181

QY 181 LYDPLYPHSMFCAGGQDQKDCSCNGDSGGPLICNGYLQGLVSFGKAPCGQVGVYTNL 240
Db 182 LYDPLYPHSMFCAGGQDQKDCSCNGDSGGPIVCNRSQGLVSMGQKCGQPGIPSYTNL 241

QY 241 CKFTWIEKTVQAS 254
Db 242 CKFTWIEKTVQAS 255

RESULT 7
Q6IE12 PRELIMINARY; PRT; 256 AA.
ID Q6IE12

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AC O6IE12;
DT 05-JUN-2004 (TrEMBLrel. 27, Created)
DT 05-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE Kallikrein 4 precursor.
GN Name=Klk4;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX PubMed=15060002; DOI=10.1101/gr.1946304;
RA Puente X.S., Lopez-Otin C.;
RL "A genomic analysis of rat proteases and protease inhibitors.";
CC -|- SIMILARITY: Belongs to peptidase family S1.
CC -|- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
DR EMBL; BN000381; CAE51907.1; -
DR HSSP; P00761; IAKS.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease; Signal.
FT SIGNAL 1 30 Potential.
FT CHAIN 31 256 kallikrein 4.
SQ SEQUENCE 256 AA; 27925 MW; 8860B91535DB3285 CRC64;

Query Match 72.9%; Score 997.5; DB 2; Length 256;
Best Local Similarity 70.8%; Pred. No. 2.5e-80;
Matches 179; Conservative 27; Mismatches 46; Indels 1; Gaps 1;

QY 1 MATAGNPGWFLGYLLVAGSLVSGSCQIINGEDCSPHSQPQWQAALVME-NELFCSGV 59
Db 2 MVTARTPWGFLGYLLVAGSLVSGSCQIINGEDCSPHSQPQWQAALFSEDAFCSGV 61

QY 60 LVHPQWLVAHCFQNSYITGLGHSLEADQEPGQSQWVEASLSVRHPEYRNPILLANDLML 119
Db 62 LVHPQWLVAHCFQNSYITGLGHSLEADQEPGQSQWVEASLSVRHPEYRNPILLANDLML 121

QY 120 IKLDESVSSEDITRSISASQCTAGNSCLVSGWGLLANGRMPTVLQCVNVSVSEVCS 179
Db 122 IKLDESVMESNTIRIPVATQCPDGTCLVSGWGLKNGKLPKSLQCVNLSVASETCR 181

QY 180 KLYDPLYHPSMFCAAGGQDQKDCNCGSGGPIVNCNRSLOGLVSMGQGCQPGIPSVYTN 239
Db 182 LLYDPVYHLSMFCAAGGQDQKDCNCGSGGPIVNCNRSLOGLVSMGQGCQPGIPSVYTN 241

QY 240 LCKFTWIEKTVQ 252
Db 242 LCKFTWNIWTIQ 254

RESULT 8
Q9Z0M1 PRELIMINARY; PRT; 255 AA.
AC Q9Z0M1;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Enamel matrix serine proteinase 1 precursor.

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GN Name=Klk4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss-Webster;
RX MEDLINE=20323211; PubMed=10863090; DOI=10.1016/S0378-1119(00)00203-1;
RA Hu J.C., Zhang C., Sun X., Yang Y., Cao X., Ryu O., Simmer J.P.;
RL "Characterization of the mouse and human PRSS17 genes, their
RT relationship to other serine proteases, and the expression of PRSS17
RT in developing mouse incisors.";
RL Gene 251:1-8(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss-Webster;
RX MEDLINE=20152522; PubMed=10890663;
RA Hu J.C.-C., Ryu O.H., Chen J.J., Uchida T., Wakida K., Murakami C.,
RA Jiang H., Qian Q., Zhang C., Ottmers V., Bartlett J.D., Simmer J.P.;
RL "Localization of Emspl expression during tooth formation and cloning
RT of mouse cDNA.";
RL J. Dent. Res. 79:70-76(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss-Webster;
RX Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -|- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AF019979; AAC98894.1; -
DR HSSP; P00760; IEZX.
DR MEROPS; S01.251; -.
DR MGD; MGI:1861379; Klk4.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease; Signal.
FT SIGNAL 1 25 Potential.
FT CHAIN 32 255 matrix serine proteinase 1.
SQ SEQUENCE 255 AA; 27488 MW; 6FD2E7DEA0660A2A CRC64;

Query Match 72.7%; Score 995; DB 2; Length 255;
Best Local Similarity 69.3%; Pred. No. 4.2e-80;
Matches 176; Conservative 31; Mismatches 47; Indels 0; Gaps 0;

QY 1 MATAGNPGWFLGYLLVAGSLVSGSCQIINGEDCSPHSQPQWQAALVME-NELFCSGVL 60
Db 2 MVTARTPWGFLGYLLVAGSLVSGSCQIINGEDCSPHSQPQWQAALFSEDAFCSGVL 61

QY 61 VHPQWLVAHCFQNSYITGLGHSLEADQEPGQSQWVEASLSVRHPEYRNPILLANDLML 120
Db 62 VHPQWLVAHCFQNSYITGLGHSLEADQEPGQSQWVEASLSVRHPEYRNPILLANDLML 121

QY 121 IKLDESVSSEDITRSISASQCTAGNSCLVSGWGLLANGRMPTVLQCVNVSVSEVCSK 180
Db 122 IKLDESVMESNTIRIPVATQCPDGTCLVSGWGLKNGKLPKSLQCVNLSVASETCRL 181

QY 181 LLYDPLYHPSMFCAAGGQDQKDCNCGSGGPIVNCNRSLOGLVSMGQGCQPGIPSVYTNL 240
Db 182 LLYDPLYHPSMFCAAGGQDQKDCNCGSGGPIVNCNRSLOGLVSMGQGCQPGIPSVYTNL 241

QY 241 LCKFTWIEKTVQAS 254
Db 242 LCKFTWNIWTIQTN 255

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RESULT 9
Q96PT0 PRELIMINARY; PRT; 195 AA.
AC Q96PT0; MEDLINE=99367447; PubMed=10438493; DOI=10.1074/jbc.274.33.23210;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Kallikrein 4 splice variant.
GN Name=KLK4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99367447; PubMed=10438493; DOI=10.1074/jbc.274.33.23210;
RA Stephenson S.A., Verity K., Ashworth L.K., Clements J.A.;
RT "Localization of a new prostate-specific antigen-related serine
RT protease gene, KLK4, is evidence for an expanded human kallikrein gene
RT family cluster on chromosome 19q13.3-13.4.";
RL J. Biol. Chem. 274:23210-23214 (1999).
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AF148532; AAL14782.1; -.
DR HSSP; Q61955; INPM.
DR GO; GO:0008236; F:serine-type peptidase activity; ISS.
DR GO; GO:0006508; P:proteolysis and peptidolysis; ISS.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN_DOM; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
KW Hydrolyase; Protease; Serine protease.
SQ SEQUENCE 195 AA; 20585 MW; EF7E96978B1515B1 CRC64;
Query Match 61.9%; Score 848; DB 2; Length 195;
Best Local Similarity 97.6%; Pred. No. 3.4e-67;
Matches 160; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 MATAGNPGWFLGYLLVAGSLVSGSCQIINGEDCSPHSQWQAALVMEELFCSGYL 60
Db 1 MATAGNPGWFLGYLLVAGSLVSGSCQIINGEDCSPHSQWQAALVMEELFCSGYL 60
QY 61 VHPQWVLSAHCFFQNSYITGLHLSLEADQEPGQWVEASLSVRHPEYRPLANDLMLI 120
Db 61 VHPQWVLSAHCFFQNSYITGLHLSLEADQEPGQWVEASLSVRHPEYRPLANDLMLI 120
QY 121 KLDESVSSEDTRISIASQCPTAGNSCLVSGWGLLANGRMPTV 164.
Db 121 KLDESVSSEDTRISIASQCPTAGNSCLVSGWGLLANGELTGV 164
RESULT 10
Q96PT1 PRELIMINARY; PRT; 159 AA.
AC Q96PT1; MEDLINE=99367447; PubMed=10438493; DOI=10.1074/jbc.274.33.23210;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Kallikrein 4 splice variant.
GN Name=KLK4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99367447; PubMed=10438493; DOI=10.1074/jbc.274.33.23210;
RA Stephenson S.A., Verity K., Ashworth L.K., Clements J.A.;
RT "Localization of a new prostate-specific antigen-related serine
RT protease gene, KLK4, is evidence for an expanded human kallikrein gene

RT family cluster on chromosome 19q13.3-13.4.";
RL J. Biol. Chem. 274:23210-23214 (1999).
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AF148532; AAL14781.1; -.
DR HSSP; Q61955; INPM.
DR GO; GO:0008236; F:serine-type peptidase activity; ISS.
DR GO; GO:0006508; P:proteolysis and peptidolysis; ISS.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN_DOM; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
KW Hydrolyase; Protease; Serine protease.
SQ SEQUENCE 159 AA; 16931 MW; 3CC66BF491B6CA5A CRC64;
Query Match 61.7%; Score 845; DB 2; Length 159;
Best Local Similarity 100.0%; Pred. No. 5e-67;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATAGNPGWFLGYLLVAGSLVSGSCQIINGEDCSPHSQWQAALVMEELFCSGYL 60
Db 1 MATAGNPGWFLGYLLVAGSLVSGSCQIINGEDCSPHSQWQAALVMEELFCSGYL 60
QY 61 VHPQWVLSAHCFFQNSYITGLHLSLEADQEPGQWVEASLSVRHPEYRPLANDLMLI 120
Db 61 VHPQWVLSAHCFFQNSYITGLHLSLEADQEPGQWVEASLSVRHPEYRPLANDLMLI 120
QY 121 KLDESVSSEDTRISIASQCPTAGNSCLVSGWGLLANG 159
Db 121 KLDESVSSEDTRISIASQCPTAGNSCLVSGWGLLANG 159
RESULT 11
Q96JD8 PRELIMINARY; PRT; 131 AA.
AC Q96JD8; MEDLINE=21398046; PubMed=11506707; DOI=10.1098/104454901750361497;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE ARMI (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=21398046; PubMed=11506707; DOI=10.1098/104454901750361497;
RA Korkmaz K.S., Korkmaz C.G., Pretlow T.G., Saatcioglu F.;
RT "Distinctly different gene structure of KLK4/KLK-ii/Prostate/ARMI
RT compared with other members of the kallikrein family - Perinuclear
RT localization, alternative cDNA forms and regulation by multiple
RT hormones";
RL DNA Cell Biol. 20:435-445 (2001).
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AF259968; AAK71704.1; -.
DR HSSP; Q61955; INPM.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; P:peptidase activity; IEA.
DR GO; GO:0004295; P:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN_DOM; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
KW Hydrolyase; Protease; Serine protease.

FT NON TER 131 131
SQ SEQUENCE 131 AA; 14107 MW; 03434B6D95AF2406 CRC64;
Query Match 49.3%; Score 675; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 5e-52;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 50 MENELFCGVLVHPQWVLSAAHCFQNSYTTGLGLHLSLEADQPGSQMVEASLSVRHPEYN 109
DB 1 MENELFCGVLVHPQWVLSAAHCFQNSYTTGLGLHLSLEADQPGSQMVEASLSVRHPEYN 60
QY 110 RPLANDMLIKLDESVESEDTIRSIASQCPAGNSCLVSGWGLIANGMPTVLQCVN 169
DB 61 RPLANDMLIKLDESVESEDTIRSIASQCPAGNSCLVSGWGLIANGMPTVLQCVN 120
QY 170 VSVVSEEVCS 179
DB 121 VSVVSEEVCS 130
RESULT 12
KLK5 HUMAN STANDARD; PRT; 293 AA.
AC Q9Y337; Q9HBG8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Kallikrein 5 precursor (EC 3.4.21.-) (Stratum corneum tryptic enzyme)
DE Kallikrein-like protein 2 (KLK-L2) (UNQ570/PROI132).
GN Name=KLK5; Synonym=SCTE;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stratum corneum;
RX MEDLINE=99445563; PubMed=10514489; DOI=10.1074/jbc.274.42.30033;
RA Brattsand M., Egelrud T.;
RT "Purification, molecular cloning, and expression of a human stratum
RT corneum trypsin-like serine protease with possible function in
RT desquamation.";
RL J. Biol. Chem. 274:30033-30040 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20118156; PubMed=10652563;
RA Yousef G.M., Luo L.-Y., Diamandis E.P.;
RT "Identification of novel human kallikrein-like genes on chromosome
RT 19q13.3-q13.4.";
RL Anticancer Res. 19:2843-2852 (1999).
RN [3]
RP SEQUENCE FROM N.A.
RX PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;
RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.;
RA Moss P., Paepel B., Wang K.;
RT "Sequencing and expression analysis of the serine protease gene
RT cluster located in chromosome 19q13 region.";
RL Gene 257:119-130 (2000).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu O., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wiewand D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";

Genome Res. 13:2265-2270 (2003).
[5]
SEQUENCE FROM N.A.
TISSUE=Ovary;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schaefer C.P., Bhat N.K.,
Altschul S.F., Zolberg B., Buetow K.H., Suetow K.H., Schaefer C.P., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Wootton K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: May be involved in desquamation.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed in skin, breast, brain and testis.
CC -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
CC subfamily.
CC
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CC
CC EMBL; AF168768; AAF03101.1; -
CC EMBL; AF135028; AAD26429.1; -
CC EMBL; AF243527; AAG33358.1; -
CC EMBL; AY359010; AAO89369.1; -
CC EMBL; BC080363; AAH08036.1; -
CC HSSP; P00760; 1EZX.
CC MEROPS; S01.017; -
CC Genew; HGNC:6366; KLK5.
CC MIM; 605643; -
CC GO; GO:0005615; C:extracellular space; TAS.
CC GO; GO:0004252; F:serine-type endopeptidase activity; NAS.
CC GO; GO:0008544; P:epidermal differentiation; TAS.
CC GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
CC InterPro; IPR009003; PeptSer_Cys.
CC InterPro; IPR001254; Peptidase_S1.
CC InterPro; IPR001314; Peptidase_S1A.
CC Pfam; PF00089; Trypsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC PROSITE; PS50240; TRYPSIN_DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; 1.
CC PROSITE; PS00135; TRYPSIN_SER; 1.
KW Glycoprotein; Hydrolase; Serine protease; Signal.
FT SIGNAL 1 22 Potential.
FT CHAIN 23 293 Kallikrein 5.
FT ACT_SITE 108 108 Charge relay system (By similarity).
FT ACT_SITE 133 133 Charge relay system (By similarity).
FT ACT_SITE 245 245 Charge relay system (By similarity).
FT DISULFID 73 206 By similarity.
FT DISULFID 93 109 By similarity.
FT DISULFID 178 279 By similarity.
FT DISULFID 185 251 By similarity.
FT DISULFID 217 231 By similarity.
FT DISULFID 241 266 By similarity.
FT CARBOHYD 69 N-linked (GlcNAc...) (Potential).
FT 69

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FT CARBOHYD 173 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 208 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 252 N-linked (GlcNAc...) (Potential).
FT CONFLICT 25 Missing (in Ref. 3).
SQ SEQUENCE 293 AA; 32020 MW; D92C92F5609E5946 CRC64;

Query Match 49.0%; Score 671; DB 1; Length 293;
Best Local Similarity 45.7%; Pred. No. 2.9e-51;
Matches 134; Conservative 47; Mismatches 72; Indels 40; Gaps 6;

QY 1 MATAGNPMGFLGYLI---LGV-----AGSLVSG----- 26
Db 1 MATARPPWVLCALITALLGLVTEHVLANDVSDHPSNTVPSSNQDLGAGAGEDARS 60
QY 27 --SCSQINGEDCSPHSQPQWAAALVME-NELFCSGVLVHPQWVLSAAHCFQNSYTIIGL 83
Db 61 DSSSSRIINGSDCMHTQWQAALLRPNQLYCGAVLHPQWLLTAACHRCXKVPFRLGH 120
QY 84 HSLLEADQEPGQOMVEASLSVRHPEYRPLANDLMLIKLDESVSSESDTIRISIASOCP 143
Db 121 YSLSPVYESGQOMFGVKSIPHPGVSHPGHSHNDLMLIKLRIRPTKDVRLNVSSHCP 180
QY 144 AGNSCLVSGWGLLANGRM--PVLQCVNVSVVSEVCSKLYDPLVHPSPMFCAGGQDQK 201
Db 181 AGTKCLVSGWGTIKSPQVHFPPKVLQCLNLSVLSQKCEDAYPRQIDDTMFCAGDKGRD 239
QY 202 SNGDSGGPLICNGYLOGLVSGKAPCGQGVGVVTVNLCKTEWIEKTVQAS 254
Db 240 SCQDGGPVPVNGSLQGLVSGWGDYPCARPNGRPGVTVNLCKTKWIOETQAN 292

RESULT 13
Q9D140 PRELIMINARY; PRT; 293 AA.
AC Q9D140;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 18-day embryo whole body cDNA, RIKEN full-length enriched
DE library, clone:1110030019 product:weakly similar to KALLIKREIN 5 (EC
DE 3.4.21.-) (STRATUM CORNEUM TRYPTIC ENZYME) (KALLIKREIN-LIKE PROTEIN 2)
DE (KIK-L2).
GN Name=1110030019Rik;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

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RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Suni N., Ishi Y., Nakamura S., Hachima M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Kanda T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multiplex capillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Koyama T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AK003996; BAB23113.1; -.
DR HSSP; P00760; 1EZX.
DR MEROPS; S01.418; -.
DR MGD; MGI:1915918; 1110030019Rik.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN_DOM; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 293 AA; 31908 MW; ED1F45D8226FE911 CRC64;

Query Match 46.6%; Score 637.5; DB 2; Length 293;
Best Local Similarity 41.5%; Pred. No. 2.8e-48;
Matches 122; Conservative 51; Mismatches 80; Indels 41; Gaps 5;

QY 1 MATAGNPMGFLGYLI---LGVAGSLVSG----- 26
Db 1 MATRGHPKWKAMATLITLVLGVSFVLGVSSCDNPSGTEPSTNRDLSTDSKSGEDT 60
QY 27 ---SCSQINGEDCSPHSQPQWAAALVME-NELFCSGVLVHPQWVLSAAHCFQNSYTIIGL 82
Db 61 RSDSSRIINGSDCQKDAQPMQWQALLGPNKLYCGAVLISPQWLLTAACHRCXKVPFRLGH 120
QY 83 LHSLEADQEPGQOMVEASLSVRHPEYRPLANDLMLIKLDESVSSESDTIRISIASOCP 142
Db 121 HHSMPVYESGQOMFGVKSIPHPGVSHPGHSHNDLMLIKLRIRPTKDVRLNVSSHCP 180
QY 143 TAGNSCLVSGWGLL--ANGRMPTVLQCVNVSVVSEVCSKLYDPLVHPSPMFCAGGQDQK 200
Db 181 TEGTRCMVSGWGTTSSSHNNPFPKVLQCLNITVLSERCKNSYPGQIDKTMFCA-GDEGR 239
QY 201 DSCNGDSGGPLICNGYLOGLVSGKAPCGQGVGVVTVNLCKTEWIEKTVQAS 254

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